GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: October 6, 2001, 17:37:52 ; Search time 2932.86 Seconds
(without alignments)
5458.535 Million cell updates/sec

Title: US-09-601-138-1
Perfect score: 1035
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1		1035	100.0	1035	9	AX020182	AX020182 Sequence
2		1035	100.0	1035	10	AX079027	AX079027 Sequence
3		1035	100.0	1113	9	AX020193	AX020193 Sequence
4		1035	100.0	1113	10	AX079028	AX079028 Sequence
5		1035	100.0	1260	9	AX020191	AX020191 Sequence
6		1035	100.0	1260	10	AX079037	AX079037 Sequence
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	16	1030.2	99.5	1035	10	AX079035 AX079035 Sequence
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ALIGNMENTS

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VERSION     AX020182.1  GI:10043973
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1035)
  AUTHORS   Fogh,J. and Gellerfors,P.
  TITLE     Method for treating acute intermittent porphyria (aip) and other
            porphyric diseases
  JOURNAL   Patent: WO 9937325-A/1 29-JUL-1999;
            FOGH JENS (DK); HEMEBIOTECH A S (DK); GELLERFORS PAER (SE)
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Best Local Similarity 100.0%; Pred. No. 4.5e-238;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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VERSION     AX079027.1  GI:13158602
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REFERENCE   1  (bases 1 to 1035)
  AUTHORS   Gellerfors,P. and Fogh,J.
  TITLE     Production of rhpbgd and new therapeutic methods for treating
            patients with acute intermittent porphyria (aip) and other
            porphyric diseases
  JOURNAL   Patent: WO 0107065-A 3 01-FEB-2001;
            Hemebiotech A/S (DK)
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REFERENCE   1  (bases 1 to 1113)
  AUTHORS   Fogh,J. and Gellerfors,P.
  TITLE     Method for treating acute intermittent porphyria (aip) and other
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  JOURNAL   Patent: WO 9937325-A 12 29-JUL-1999;
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DEFINITION  Sequence 4 from Patent WO0107065.
ACCESSION   AX079028
VERSION     AX079028.1  GI:13158603
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1113)
  AUTHORS   Gellerfors,P. and Fogh,J.
  TITLE     Production of rhpbgd and new therapeutic methods for treating
            patients with acute intermittent porphyria (aip) and other
            porphyric diseases
  JOURNAL   Patent: WO 0107065-A 4 01-FEB-2001;
            Hemebiotech A/S (DK)

FEATURES             Location/Qualifiers
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ORIGIN


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LOCUS       AX020191     1260 bp    DNA              PAT       07-SEP-2000
DEFINITION  Sequence 10 from Patent WO9937325.
ACCESSION   AX020191
VERSION     AX020191.1  GI:10043982
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1260)
  AUTHORS   Fogh,J. and Gellerfors,P.
  TITLE     Method for treating acute intermittent porphyria (aip) and other
            porphyric diseases
  JOURNAL   Patent: WO 9937325-A 10 29-JUL-1999;
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DEFINITION  Sequence 13 from Patent WO0107065.
ACCESSION   AX079037
VERSION     AX079037.1  GI:13158612
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SOURCE      human.
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REFERENCE   1  (bases 1 to 1260)
  AUTHORS   Gellerfors,P. and Fogh,J.
  TITLE     Production of rhpbgd and new therapeutic methods for treating
            patients with acute intermittent porphyria (aip) and other
            porphyric diseases
  JOURNAL   Patent: WO 0107065-A 13 01-FEB-2001;
            Hemebiotech A/S (DK)
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VERSION     AX020190.1  GI:10043981
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SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3988)
  AUTHORS   Fogh,J. and Gellerfors,P.
  TITLE     Method for treating acute intermittent porphyria (aip) and other
            porphyric diseases
  JOURNAL   Patent: WO 9937325-A 9 29-JUL-1999;
            FOGH JENS (DK); HEMEBIOTECH A S (DK); GELLERFORS PAER (SE)
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Qy   1021 aacgatgcccattaa 1035
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DEFINITION  Sequence 12 from Patent WO0107065.
ACCESSION   AX079036
VERSION     AX079036.1  GI:13158611
KEYWORDS    .
SOURCE      human.
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REFERENCE   1  (bases 1 to 3988)
  AUTHORS   Gellerfors,P. and Fogh,J.
  TITLE     Production of rhpbgd and new therapeutic methods for treating
            patients with acute intermittent porphyria (aip) and other
            porphyric diseases
  JOURNAL   Patent: WO 0107065-A 12 01-FEB-2001;
            Hemebiotech A/S (DK)
FEATURES             Location/Qualifiers
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ORIGIN


  Query Match           100.0%;  Score 1035;  DB 10;  Length 3988;
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RESULT   9
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LOCUS       AX020183     1035 bp    DNA              PAT       07-SEP-2000
DEFINITION  Sequence 2 from Patent WO9937325.
ACCESSION   AX020183
VERSION     AX020183.1  GI:10043974
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1035)
  AUTHORS   Fogh,J. and Gellerfors,P.
  TITLE     Method for treating acute intermittent porphyria (aip) and other
            porphyric diseases
  JOURNAL   Patent: WO 9937325-A 2 29-JUL-1999;
            FOGH JENS (DK); HEMEBIOTECH A S (DK); GELLERFORS PAER (SE)
FEATURES             Location/Qualifiers
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BASE COUNT      250 a    271 c    303 g    211 t
ORIGIN


  Query Match             99.8%;  Score 1033.4;  DB 9;  Length 1035;
  Best Local Similarity   99.9%;  Pred. No. 1.1e-237;
  Matches 1034;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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LOCUS       AX020184     1035 bp    DNA             PAT       07-SEP-2000
DEFINITION  Sequence 3 from Patent WO9937325.
ACCESSION   AX020184
VERSION     AX020184.1  GI:10043975
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1035)
  AUTHORS   Fogh,J. and Gellerfors,P.
  TITLE     Method for treating acute intermittent porphyria (aip) and other
            porphyric diseases
  JOURNAL   Patent: WO 9937325-A 3 29-JUL-1999;
            FOGH JENS (DK); HEMEBIOTECH A S (DK); GELLERFORS PAER (SE)
FEATURES             Location/Qualifiers
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ORIGIN


  Query Match             99.8%;  Score 1033.4;  DB 9;  Length 1035;
  Best Local Similarity   99.9%;  Pred. No. 1.1e-237;
  Matches 1034;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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RESULT  11
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LOCUS       AX079029     1035 bp    DNA             PAT       22-FEB-2001
DEFINITION  Sequence 5 from Patent WO0107065.
ACCESSION   AX079029
VERSION     AX079029.1  GI:13158604
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1035)
  AUTHORS   Gellerfors,P. and Fogh,J.
  TITLE     Production of rhpbgd and new therapeutic methods for treating
            patients with acute intermittent porphyria (aip) and other
            porphyric diseases
  JOURNAL   Patent: WO 0107065-A 5 01-FEB-2001;
            Hemebiotech A/S (DK)
FEATURES             Location/Qualifiers
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ORIGIN


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Qy    661 ctgcacgatcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctg 720
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Db    661 CTGCACGATCCCGAGACTCTGCTTCGCTGCATCGCTGAAAGGGCCTTCCTGAGGCACCTG 720

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Qy    781 ctgactggaggagtctggagtctagacggctcagatagcatacaagagaccatgcaggct 840
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RESULT  12
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DEFINITION  Sequence 6 from Patent WO0107065.
ACCESSION   AX079030
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VERSION     AX079030.1  GI:13158605
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE   1  (bases 1 to 1035)
  AUTHORS   Gellerfors,P. and Fogh,J.
  TITLE     Production of rhpbgd and new therapeutic methods for treating
            patients with acute intermittent porphyria (aip) and other
            porphyric diseases
  JOURNAL   Patent: WO 0107065-A 6 01-FEB-2001;
            Hemebiotech A/S (DK)
FEATURES             Location/Qualifiers
     source          1. .1035
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BASE COUNT      250 a    271 c    303 g    211 t
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Query Match 99.8%; Score 1033.4; DB 10; Length 1035;
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Matches 1034; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT  13
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DEFINITION  Sequence 6 from Patent WO9937325.
ACCESSION   AX020187
VERSION     AX020187.1  GI:10043978
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1035)
  AUTHORS   Fogh,J. and Gellerfors,P.
  TITLE     Method for treating acute intermittent porphyria (aip) and other
            porphyric diseases
  JOURNAL   Patent: WO 9937325-A 6 29-JUL-1999;
            FOGH JENS (DK); HEMEBIOTECH A S (DK); GELLERFORS PAER (SE)
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Query Match 99.7%; Score 1031.8; DB 9; Length 1035;
Best Local Similarity 99.8%; Pred. No. 2.7e-237;
Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DEFINITION Sequence 9 from Patent WO0107065.
ACCESSION AX079033
VERSION AX079033.1 GI:13158608
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1035)
AUTHORS Gellerfors,P. and Fogh,J.
TITLE Production of rhpbgd and new therapeutic methods for treating patients with acute intermittent porphyria (aip) and other porphyric diseases
JOURNAL Patent: WO 0107065-A 9 01-FEB-2001;
Hemebiotech A/S (DK)
FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
BASE COUNT 250 a 270 c 303 g 212 t
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Query Match 99.7%; Score 1031.8; DB 10; Length 1035;
Best Local Similarity 99.8%; Pred. No. 2.7e-237;
Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DEFINITION  Sequence 8 from Patent WO9937325.
ACCESSION   AX020189
VERSION     AX020189.1  GI:10043980
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1035)
  AUTHORS   Fogh,J. and Gellerfors,P.
  TITLE     Method for treating acute intermittent porphyria (aip) and other
            porphyric diseases
  JOURNAL   Patent: WO 9937325-A 8 29-JUL-1999;
            FOGH JENS (DK); HEMEBIOTECH A S (DK); GELLERFORS PAER (SE)
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  Best Local Similarity   99.7%;  Pred. No. 6.4e-237;
  Matches 1032;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 atgagagtgattcgcgtgggtacccgcaagagccagcttgctcgcatacagacggacagt 60
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Db      1 ATGAGAGTGATTCGCGTGGGTACCCGCAAGAGCCAGCTTGCTCGCATACAGACGGACAGT 60

Qy     61 gtggtggcaacattgaaagcctcgtaccctggcctgcagtttgaaatcattgctatgtcc 120
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Db     61 GTGGTGGCAACATTGAAAGCCTCGTACCCTGGCCTGCAGTTTGAAATCATTGCTATGTCC 120

Qy    121 accacaggggacaagattcttgatactgcactctctaagattggagagaaaagcctgttt 180
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Db    121 ACCACAGGGGACAAGATTCTTGATACTGCACTCTCTAAGATTGGAGAGAAAAGCCTGTTT 180

Qy    181 accaaggagcttgaacatgccctggagaagaatgaagtggacctggttgttcactccttg 240
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Qy    241 aaggacctgcccactgtgcttcctcctggcttcaccatcggagccatctgcaagcgggaa 300
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Qy    301 aaccctcatgatgctgttgtctttcacccaaaatttgttgggaagaccctagaaaccctg 360
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Qy    361 ccagagaagagtgtggtgggaaccagctccctgcgaagagcagcccagctgcagagaaag 420
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Qy    421 ttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttcggaagctg 480
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Db    421 TTCCCGCATCTGGAGTTCAGGAGTATTCGGGGAAACCTCAACACCCGGCTTCGGAAGCTG 480

Qy    481 gacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatgggc 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GACGAGCAGCAGGAGTTCAGTGCCATCATCCTGGCAACAGCTGGCCTGCAGCGCATGGGC 540

Qy    541 tggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctgtgggccag 600
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGGCACAACCGGGTGGGGCAGATCCTGCACCCTGAGGAATGCATGTATGCTGTGGGCCAG 600

Qy    601 ggggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtg 660
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Db    601 GGGGCCTTGGGCGTGGAAGTGCGAGCCAAGGACCAGGACATCTTGGATCTGGTGGGTGTG 660

Qy    661 ctgcacgatcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctg 720
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Db    661 CTGCACGATCCCGAGACTCTGCTTCGCTGCATCGCTGAAAGGGCCTTCCTGAGGCACCTG 720

Qy    721 gaaggaggctgcagtgtgccagtagccgtgcatacagctatgaaggatgggcaactgtac 780
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Qy    781 ctgactggaggagtctggagtctagacggctcagatagcatacaagagaccatgcaggct 840
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Db    781 CTGACTGGAGGAGTCTGGAGTCTAGACGGCTCAGATAGCATACAAGAGACCATGCAGGCC 840

Qy    841 accatccatgtccctgcccagcatgaagatggccctgaggatgacccacagttggtaggc 900
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ACCATCCATGTCCCTACCCAGCATGAAGATGGCCCTGAGGATGACCCACAGTTGGTAGGC 900

Qy    901 atcactgctcgtaacattccacgagggccccagttggctgcccagaacttgggcatcagc 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ATCACTGCTCGTAACATTCCACGAGGGCCCCAGTTGGCTGCCCAGAACTTGGGCATCAGC 960

Qy    961 ctggccaacttgttgctgagcaaaggagccaaaaacatcctggatgttgcacggcaattg 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CTGGCCAACTTGTTGCTGAGCAAAGGAGCCAAAAACATCCTGGATGTTGCACGGCAATTG 1020

Qy   1021 aacgatgcccattaa 1035
          ||||||||||||||||
Db   1021 AACGATGCCCATTAA 1035
```

```
Search completed: October  6, 2001, 18:32:02
Job time: 3250 sec
```

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: October 6, 2001, 17:37:52 ; Search time 1970.35 Seconds
(without alignments)
4965.465 Million cell updates/sec

Title: US-09-601-138-1
Perfect score: 1035
Sequence: 1 atgagagtgattcgcgtggg.....aattgaacgatgcccattaa 1035

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: gb_est9:*
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256: gb_gss35:*
257: gb_gss36:*
258: gb_gss37:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	837.4	80.9	882	105	AL524270	AL524270 AL524270
2	804.8	77.8	1036	105	AL520285	AL520285 AL520285
3	728.4	70.4	904	152	BG337601	BG337601 602435148
c 4	711.4	68.7	949	106	AL561865	AL561865 AL561865
5	698.2	67.5	878	105	AL516000	AL516000 AL516000
6	690.4	66.7	942	106	AL557370	AL557370 AL557370
c 7	682	65.9	838	106	AL579416	AL579416 AL579416
8	671.4	64.9	804	137	BE547860	BE547860 601074758
c 9	659.2	63.7	919	105	AL520284	AL520284 AL520284
10	650.4	62.8	801	143	BF035760	BF035760 601458755
11	649.2	62.7	1136	137	BE561357	BE561357 601344923
12	646.4	62.5	835	154	BG469642	BG469642 602533692
13	635.6	61.4	908	105	AL520223	AL520223 AL520223
c 14	628.8	60.8	941	106	AL561775	AL561775 AL561775
15	610.2	59.0	812	108	AU132868	AU132868 AU132868
c 16	602.2	58.2	746	106	AL562330	AL562330 AL562330
17	586	56.6	695	136	BE514746	BE514746 601317044
18	579.8	56.0	1087	137	BE561038	BE561038 601344655
19	573	55.4	970	172	BF971877	BF971877 602240467
20	568.2	54.9	883	107	AU118927	AU118927 AU118927
c 21	557	53.8	755	105	AL515999	AL515999 AL515999
22	549.4	53.1	693	140	BE795040	BE795040 601592839
23	548	52.9	869	141	BE870723	BE870723 601448575
24	544.8	52.6	840	18	AI325891	AI325891 mg10e04.y
25	543	52.5	847	153	BG421936	BG421936 602449682
26	539.8	52.2	795	141	BE905261	BE905261 601499109
27	522.8	50.5	538	172	BG025746	BG025746 602274731
28	515.2	49.8	807	108	AU143511	AU143511 AU143511
29	509	49.2	963	174	BG180160	BG180160 602329751
30	506	48.9	666	167	BE396412	BE396412 601288795
31	502.8	48.6	776	106	AL531360	AL531360 AL531360
32	491.4	47.5	873	152	BG336990	BG336990 602434444
33	490.8	47.4	1090	175	BG257063	BG257063 602370616
34	487.4	47.1	619	119	AW701590	AW701590 uq88b01.y
35	485.8	46.9	807	107	AU120403	AU120403 AU120403
36	484.2	46.8	826	146	BF213889	BF213889 601848118
37	483.8	46.7	1087	152	BG338518	BG338518 602436243
c 38	482.2	46.6	1044	139	BE739550	BE739550 601556493
39	479.4	46.3	849	152	BG339222	BG339222 602437086
c 40	474.6	45.9	648	106	AL564037	AL564037 AL564037
41	472	45.6	655	190	W61658	W61658 md82a02.r1
42	464	44.8	893	137	BE561477	BE561477 601346541
43	458.6	44.3	741	10	AA672024	AA672024 vl03g02.r
44	453.4	43.8	968	141	BE889503	BE889503 601512410
45	450.8	43.6	797	15	AI048619	AI048619 ud64a04.y

ALIGNMENTS

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RESULT  1
AL524270
LOCUS       AL524270      882 bp    mRNA            EST       13-FEB-2001
DEFINITION  AL524270 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC002YJ01 5
            prime, mRNA sequence.
ACCESSION   AL524270
VERSION     AL524270.1  GI:12787763
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 882)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="CS0DC002YJ01"
                     /clone_lib="LTI_NFL003_NBC3"
                     /sex="male"
                     /tissue_type="neuroblastoma cells"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector.  Library was normalized. Library was constructed
                     by Life Technologies.  Contact : Feng Liang Life
                     Technologies, a division of Invitrogen 9800 Medical Center
                     Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
                     8371 Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      205 a    236 c    262 g    178 t      1 others
ORIGIN
```

Query Match 80.9%; Score 837.4; DB 105; Length 882;
Best Local Similarity 99.2%; Pred. No. 3.4e-213;
Matches 852; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

```
Qy    175 ctgtttaccaaggagcttgaacatgccctggagaagaatgaagtggacctggttgttcac 234
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Db      1 CTGTTTACCAAGGAGCTTGAACATGCCCTGGAGAAGAATGAAGTGGACCTGGTTGTTCAC 60

Qy    235 tccttgaaggacctgcccactgtgcttcctcctggcttcaccatcggagccatctgcaag 294
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    295 cgggaaaaccctcatgatgctgttgtctttcacccaaaatttgttgggaagaccctagaa 354
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    355 accctgccagagaagagtgtggtgggaaccagctccctgcgaagagcagcccagctgcag 414
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Qy    415 agaaagttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttcgg 474
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Qy    475 aagctggacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgc 534
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Qy    535 atgggctggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctgtg 594
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Qy    715 cacctggaaggaggctgcagtgtgccagtagccgtgcatacagctatgaaggatgggcaa 774
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Qy    775 ctgtacctgactggaggagtctggagtctagacggctcagatagcatacaagagaccatg 834
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Qy    835 caggctaccatccatgtccctgcccagcatgaagatggccctgaggatgacccacagttg 894
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Db    660 CAGGCTACCATCCATGTCCCTGCCCAGCATGAAGATGGCCCTGAGGATGACCCACAGTTG 719

Qy    895 gtaggcatcactgctcgtaacattccacgagggccccagttggctgcccagaacttgggc 954
          ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    720 GTAGGCATCACTGCTCGTAACAATCCACGAGGGCCCCAGTTGGCTGCCCAGAACTTGGGC 779

Qy    955 atcagcctggccaacttgttgctgagcaaaggagccaaaaacatcctggatgttgcacgg 1014
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    780 ATCAGCCTGGCCAACTTGTTGCTGAGCAAAGGAGCCAAAAACATCCTGGATGTTGCACGG 839

Qy   1015 caattgaacgatgcccatt 1033
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Db    840 CAGCCTAACGATGCCCATT 858
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RESULT   2
AL520285
LOCUS       AL520285      1036 bp    mRNA            EST       13-FEB-2001
DEFINITION  AL520285 LTI_NFL004_NBC2 Homo sapiens cDNA clone CS0DB006YG07 5
            prime, mRNA sequence.
ACCESSION   AL520285
VERSION     AL520285.1  GI:12783778
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1036)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .1036
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DB006YG07"
                     /clone_lib="LTI_NFL004_NBC2"
                     /sex="male"
                     /tissue_type="neuroblastoma cells"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector.  Library was normalized. Library was constructed
                     by Life Technologies.  Contact : Feng Liang Life
                     Technologies, a division of Invitrogen 9800 Medical Center
                     Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
                     8371 Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      243 a    282 c    310 g    200 t      1 others
ORIGIN
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  Query Match           77.8%;  Score 804.8;  DB 105;  Length 1036;
  Best Local Similarity  99.1%;  Pred. No. 1.8e-204;
  Matches  850;  Conservative    1;  Mismatches    3;  Indels    4;  Gaps    4;

Qy      1 atgagagtgattcgcgtgggtacccgcaagagccagcttgctcgcatacagacggacagt 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    179 ATGAGAGTGATTCGCGTGGGTACCCGCAAGAGCCAGCTTGCTCGCATACAGACGGACAGT 238

Qy     61 gtggtggcaacattgaaagcctcgtaccctggcctgcagtttgaaatcattgctatgtcc 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    239 GTGGTGGCAACATTGAAAGCCTCGTACCCTGGCCTGCAGTTTGAAATCATTGCTATGTCC 298
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Qy    121 accacaggggacaagattcttgatactgcactctctaagattggagagaaaagcctgttt 180
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Db    299 ACCACAGGGGACAAGATTCTTGATACTGCACTCTCTAAGATTGGAGAGAAAAGCCTGTTT 358

Qy    181 accaaggagcttgaacatgccctggagaagaatgaagtggacctggttgttcactccttg 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    359 ACCAAGGAGCTTGAACATGCCCTGGAGAAGAATGAAGTGGACCTGGTTGTTCACTCCTTG 418

Qy    241 aaggacctgcccactgtgcttcctcctggcttcaccatcggagccatctgcaagcgggaa 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    419 AAGGACCTGCCCACTGTGCTTCCTCCTGGCTTCACCATCGGAGCCATCTGCAAGCGGGAA 478

Qy    301 aaccctcatgatgctgttgtctttcacccaaaatttgttgggaagaccctagaaaccctg 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    479 AACCCTCATGATGCTGTTGTCTTTCACCCAAAATTTGTTGGGAAGACCCTAGAAACCCTG 538

Qy    361 ccagagaagagtgtggtgggaaccagctccctgcgaagagcagcccagctgcagagaaag 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    539 CCAGAGAAGAGTGTGGTGGGAACCAGCTCCCTGCGAAGAGCAGCCCAGCTGCAGAGAAAG 598

Qy    421 ttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttcggaagctg 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    599 TTCCCGCATCTGGAGTTCAGGAGTATTCGGGGAAACCTCAACACCCGGCTTCGGAAGCTG 658

Qy    481 gacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatgggc 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    659 GACGAGCAGCAGGAGTTCAGTGCCATCATCCTGGCAACAGCTGGCCTGCAGCGCATGGGC 718

Qy    541 tggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctgtgggccag 600
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    719 TGGCACAACCGGGTGGGGCAGATCCTGCACCCTGAGGAATGCATGTATGCTGTGGGCCAG 778

Qy    601 ggggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtg 660
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Db    779 GGGGCCTTGGGCGTGGAAGTGCGAGCCAAGGACCAGGACATCTTGGATCTGGTGGGTGTG 838

Qy    661 ctgcacgatcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctg 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    839 CTGCACGATCCCGAGACTCTGCTTCGCTGCATCGCTGAAAGGGCCTTCCTGAGGCA-CTG 897

Qy    721 gaaggaggctgcagtgtgccagtagccgtgcatacagctatgaaggatgggcaactgtac 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    898 GAAGGAGGCTGCAGTGTGCCAGTAGCCGTGCATACAGCTATGAAGGATGGGCAACTGTAC 957

Qy    781 ctgactggaggagtctggagtctagacggctcagatagcatacaagagaccatgcaggct 840
          |||||||||||||||||||||||| |:|||||||||||||||||| ||||||||||
Db    958 CTGACTGGAGGAGTCTGGAGTCTAGAC-GSTCAGATAGCATACAAGAGA-CATGCAGGCT 1015

Qy    841 accatccatgtccctgcc 858
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Db   1016 A-CATCCATGTCCCGCCC 1032
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RESULT   3
BG337601
LOCUS       BG337601      904 bp    mRNA            EST       27-FEB-2001
DEFINITION  602435148F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4553315 5',
            mRNA sequence.
ACCESSION   BG337601
VERSION     BG337601.1  GI:13144039
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 904)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
```

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            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM1250  row: o  column: 12
           High quality sequence stop: 768.
FEATURES             Location/Qualifiers
     source          1. .904
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4553315"
                     /clone_lib="NIH_MGC_46"
                     /tissue_type="leiomyosarcoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using  ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."
BASE COUNT      212 a    234 c    285 g    171 t      2 others
ORIGIN


  Query Match             70.4%;  Score 728.4;  DB 152;  Length 904;
  Best Local Similarity   98.6%;  Pred. No. 4.8e-184;
  Matches  765;  Conservative    0;  Mismatches    8;  Indels    3;  Gaps    3;

Qy    155 ctaagattggagagaaaagcctgtttaccaaggagcttgaacatgccctggagaagaatg 214
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 CTAAGATTGGAGAGAAAAGCCTGTTTACCAAGGAGCTTGAACATGCCCTGGAGAAGAATG 61

Qy    215 aagtggacctggttgttcactccttgaaggacctgcccactgtgcttcctcctggcttca 274
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 AAGTGGACCTGGTTGTTCACTCCTTGAAGGACCTGCCCACTGTGCTTCCTCCTGGCTTCA 121

Qy    275 ccatcggagccatctgcaagcgggaaaaccctcatgatgctgttgtctttcacccaaaat 334
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122 CCATCGGAGCCATCTGCAAGCGGGAAAACCCTCATGATGCTGTTGTCTTTCACCCAAAAT 181

Qy    335 ttgttgggaagaccctagaaaccctgccagagaagagtgtggtgggaaccagctccctgc 394
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    182 TTGTTGGGAAGACCCTAGAAACCCTGCCAGAGAAGAGTGTGGTGGGAACCAGCTCCCTGC 241

Qy    395 gaagagcagcccagctgcagagaaagttcccgcatctggagttcaggagtattcggggaa 454
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Db    242 GAAGAGCAGCCCAGCTGCAGAGAAAGTTCCCGCATCTGGAGTTCAGGAGTATTCGGGGAA 301

Qy    455 acctcaacacccggcttcggaagctggacgagcagcaggagttcagtgccatcatcctgg 514
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    302 ACCTCAACACCCGGCTTCGGAAGCTGGACGAGCAGCAGGAGTTCAGTGCCATCATCCTGG 361

Qy    515 caacagctggcctgcagcgcatgggctggcacaaccgggttgggcagatcctgcaccctg 574
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Db    362 CAACAGCTGGCCTGCAGCGCATGGGCTGGCACAACCGGGTGGGGCAGATCCTGCACCCTG 421

Qy    575 aggaatgcatgtatgctgtgggccaggggccttgggcgtggaagtgcgagccaaggacc 634
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Db    422 AGGAATGCATGTATGCTGTGGGCCAGGGGGCCTTGGGCGTGGAAGTGCGAGCCAAGGACC 481

Qy    635 aggacatcttggatctggtgggtgtgctgcacgatcccgagactctgcttcgctgcatcg 694
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Db    482 AGGACATCTTGGATCTGGTGGGTGTGCTGCACGATCCCGAGACTCTGCTTCGCTGCATCG 541

Qy    695 ctgaaagggccttcctgaggcacctggaaggaggctgcagtgtgccagtagccgtgcata 754
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    542 CTGAAAGGGCCTTCCTGAGGCACCTGGAAGGAGGCTGCAGTGTGCCAGTAGCCGTGCATA 601

Qy    755 cagctatgaaggatgggcaactgtacctgactggaggagtctggagtctagacggctcag 814
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| | ||||
Db    602 CAGCTATGAAGGATGGGCAACTGTACCTGACTGGAGGAGTCTGGAGTCTAGACNGGTCAG 661

Qy    815 atagcatacaagagaccatgcaggctaccatccatgtccctgcccagcatgaagatggcc 874
          |||||||||||||||||||||||||| ||||||||| |||| ||||||||||||||| |
Db    662 ATAGCATACAAGAGACCATGCAGGCTA-CATCCATGTTCCTGTCCAGCATGAAGATGGNC 720

Qy    875 ctgaggatgacccacagttggtaggcatcactgctcgtaacattccacgagggccc 930
          |||||||||| |||||||||||||| |||||| |||||||||||||||||| |||
Db    721 CTGAGGATGA-CCACAGTTGGTAGGC-TCACTGGTCGTAACATTCCACGAGGCCCC 774


RESULT   4
AL561865/c
LOCUS       AL561865      949 bp    mRNA            EST       16-FEB-2001
DEFINITION  AL561865 LTI_NFL004_NBC2 Homo sapiens cDNA clone CS0DB006YI03 3
            prime, mRNA sequence.
ACCESSION   AL561865
VERSION     AL561865.1  GI:12909719
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 949)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .949
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                     /db_xref="taxon:9606"
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                     /clone_lib="LTI_NFL004_NBC2"
                     /sex="male"
                     /tissue_type="neuroblastoma cells"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector.  Library was normalized. Library was constructed
                     by Life Technologies.  Contact : Feng Liang Life
                     Technologies, a division of Invitrogen 9800 Medical Center
                     Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
                     8371 Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      196 a    277 c    265 g    207 t      4 others
ORIGIN


  Query Match             68.7%;  Score 711.4;  DB 106;  Length 949;
  Best Local Similarity   98.6%;  Pred. No. 1.7e-179;
  Matches  756;  Conservative    3;  Mismatches    4;  Indels    4;  Gaps    4;

Qy    269 gcttcaccatcggagccatctgcaagcgggaaaaccctcatgatgctgttgtctttcacc 328
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Db    940 GCTTCACCATCGGAGCCATCTGMAAGC-GGAAAACCCTCATGATGCTGTTGTC-TTCACC 883

Qy    329 caaaatttgttgggaagaccctagaaaccctgccagagaagagtgtggtgggaaccagct 388
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    882 CAAAATTTGTT-GGAAGACCCTAGAAACCCTGCCAGAGAAGAGTGTGGTGGGAACCAGCT 824

Qy    389 ccctgcgaagagcagcccagctgcagagaaagttcccgcatctggagttcaggagtattc 448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    823 CCCTGCGAAGAGCAGCCCAGCTGCAGAGAAAGTTCCCGCATCTGGAGTTCAGGAGTATTC 764

Qy    449 ggggaaacctcaacacccggcttcggaagctggacgagcagcaggagttcagtgccatca 508
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Db    763 GGGGAAACCTCAACACCCGGCTTCGGAAGCTGGACGAGCAGCAGGAGTTCAGTGCCATCA 704

Qy    509 tcctggcaacagctggcctgcagcgcatgggctggcacaaccgggttgggcagatcctgc 568
          ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    703 TCCTGGCAACAGCTGGCCTGCAGCGCATGGGCTGGCACAACCGGGTGGGGCAGATCCTGC 644

Qy    569 accctgaggaatgcatgtatgctgtgggccaggggccttgggcgtggaagtgcgagcca 628
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Db    643 ACCCTGAGGAATGCATGTATGCTGTGGGCCAGGGGGCCTTGGGCGTGGAAGTGCGAGCCA 584

Qy    629 aggaccaggacatcttggatctggtgggtgtgctgcacgatcccgagactctgcttcgct 688
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Db    583 AGGACCARGACATCTTRGATCTGGTGGGTGTGCTGCACGATCCCGAGACTCT-CTTCGCT 525

Qy    689 gcatcgctgaaagggccttcctgaggcacctggaaggaggctgcagtgtgccagtagccg 748
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Db    524 GCATCGCTGAAAGGGCCTTCCTGAGGCACCTGGAAGGAGGCTGCAGTGTGCCAGTAGCCG 465

Qy    749 tgcatacagctatgaaggatgggcaactgtacctgactggaggagtctggagtctagacg 808
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Db    464 TGCATACAGCTATGAAGGATGGGCAACTGTACCTGACTGGAGGAGTCTGGAGTCTAGACG 405

Qy    809 gctcagatagcatacaagagaccatgcaggctaccatccatgtccctgcccagcatgaag 868
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Db    404 GCTCAGATAGCATACAAGAGACCATGCAGGCTACCATCCATGTCCCTGCCCAGCATGAAG 345

Qy    869 atggccctgaggatgacccacagttggtaggcatcactgctcgtaacattccacgagggc 928
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Db    344 ATGGCCCTGAGGATGACCCACAGTTGGTAGGCATCACTGCTCGTAACATTCCACGAGGGC 285

Qy    929 cccagttggctgcccagaacttgggcatcagcctggccaacttgttgctgagcaaaggag 988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    284 CCCAGTTGGCTGCCCAGAACTTGGGCATCAGCCTGGCCAACTTGTTGCTGAGCAAAGGAG 225

Qy    989 ccaaaaacatcctggatgttgcacggcaattgaacgatgcccattaa 1035
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Db    224 CCAAAAACATCCTGGATGTTGCACGGCAGCTTAACGATGCCCATTAA 178
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RESULT   5
AL516000
LOCUS       AL516000      878 bp    mRNA            EST       13-FEB-2001
DEFINITION  AL516000 LTI_NFL011_NBC1 Homo sapiens cDNA clone CS0DA005YC03 5
            prime, mRNA sequence.
ACCESSION   AL516000
VERSION     AL516000.1  GI:12779493
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 878)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .878
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                     /db_xref="taxon:9606"
                     /clone="CS0DA005YC03"
                     /clone_lib="LTI_NFL011_NBC1"
                     /sex="male"
                     /tissue_type="neuroblastoma cells"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector.  Library is not normalized, but is the control for
                     the normalized libraries. Library was constructed by Life
                     Technologies.  Contact : Feng Liang Life Technologies, a
                     division of Invitrogen 9800 Medical Center Drive Rockville
                     , Maryland 20850, USA Fax : (1) 301 610 8371 Email :
                     fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      200 a    235 c    264 g    173 t      6 others
ORIGIN
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  Best Local Similarity   94.3%;  Pred. No. 5.6e-176;
  Matches  746;  Conservative    4;  Mismatches    2;  Indels   39;  Gaps    1;

Qy     36 gcttgctcgcatacagacggacagtgtggtggcaacattgaaagcctcgtaccctggcct 95
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    127 GCTTGCTCGCATACAGACGGACAGTGTGGTGGCAACATTGAAAGCCTCGTACCCTGGCCT 186

Qy     96 gcagtttgaaatcattgctatgtccaccacaggggacaagattcttgatactgcactctc 155
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Db    187 GCAGTTTGAAATCATTGCTATGTCCACCACAGGGGACAAGATTYTTGATACTGCACTCTC 246

Qy    156 taagattggagagaaaagcctgtttaccaaggagcttgaacatgccctggagaagaatga 215
          |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    247 TAARATTGGAGAGAAAAGCCTGTTTACCAAGGAGCTTGAACATGCCCTGGAGAAGAATGA 306

Qy    216 agtggacctggttgttcactccttgaaggacctgcccactgtgcttcctcctggcttcac 275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    307 AGTGGACCTGGTTGTTCACTCCTTGAAGGACCTGCCCACTGTGCTTCCTCCTGGCTTCAC 366

Qy    276 catcggagccatctgcaagcgggaaaaccctcatgatgctgttgtctttcacccaaaatt 335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    367 CATCGGAGCCATCTGCAAGCGGGAAAACCCTCATGATGCTGTTGTCTTTCACCCAAAATT 426

Qy    336 tgttgggaagaccctagaaaccctgccagagaagagtgtggtgggaaccagctccctgcg 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    427 TGTTGGGAAGACCCTAGAAACCCTGCCAGAGAAGAGTGTGGTGGGAACCAGCTCCCTGCG 486

Qy    396 aagagcagcccagctgcagagaaagttcccgcatctggagttcaggagtattcggggaaa 455
          |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    487 AAGAGCAGCCCAGCTGCAGAGAAAGTTCCCGCATCTGGAGTACAGGAGTATTCGGGGAAA 546

Qy    456 cctcaacacccggcttcggaagctggacgagcagcaggagttcagtgccatcatcctggc 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    547 CCTCAACACCCGGCTTCGGAAGCTGGACGAGCAGCAGGAGTTCAGTGCCATCATCCTGGC 606

Qy    516 aacagctggcctgcagcgcatgggctggcacaaccgggttgggcagatcctgcaccctga 575
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Db    607 AACAGCTGGCCTGCAGCGCATGGGCTGGCACAACCGG---------------------- 643

Qy    576 ggaatgcatgtatgctgtgggccaggggccttgggcgtggaagtgcgagccaaggacca 635
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Db    644 ---------------GTGGGGCAGGGGGCCTTGGGCGTGGAAGTGCGAGCCAAGGACCA 687

Qy    636 ggacatcttggatctggtgggtgtgctgcacgatcccgagactctgcttcgctgcatcgc 695
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Db    688 GGACATCTTGGATCTGGTGGGTGTGCTGCACGATCCCGAGACTCTGCTTCGCTGCATCGC 747

Qy    696 tgaaagggccttcctgaggcacctggaaggaggctgcagtgtgccagtagccgtgcatac 755
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Db    748 TGAAAGGGCCTTCCTGAGGCACCTGGAAGGAGGCTGCAGTGTGCCAGTWGCCGTGCATAC 807

Qy    756 agctatgaaggatgggcaactgtacctgactggaggagtctggagtctagacggctcaga 815
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Db    808 AGCTATGAAGGATGGGCAACTGTACCTGACTGGAGGAGTCTGGAGTCTAGACGGCTCAGA 867

Qy    816 tagcatacaag 826
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Db    868 TAGCATAMAAG 878
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RESULT   6
AL557370
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LOCUS       AL557370      942 bp    mRNA            EST       16-FEB-2001
DEFINITION  AL557370 LTI_FL012_TC1 Homo sapiens cDNA clone CS0DH004YP13 5 prime
            , mRNA sequence.
ACCESSION   AL557370
VERSION     AL557370.1  GI:12900909
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 942)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
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                     /clone_lib="LTI_FL012_TC1"
                     /tissue_type="T cells from T cell leukemia"
                     /lab_host="DH10B"
                     /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-stranded cDNA was digested with Not I and cloned
                     into the Not I and Eco RV sites of the pCMVSPORT 6 vector.
                     Library was constructed by Life Technologies. Contact :
                     Feng Liang Life Technologies, a division of Invitrogen
                     9800 Medical Center Drive Rockville, Maryland 20850, USA
                     Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      216 a    258 c    284 g    183 t      1 others
ORIGIN
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  Query Match             66.7%;  Score 690.4;  DB 106;  Length 942;
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Qy       1 atgagagtgattcgcgtgggtacccgcaagagccagcttgctcgcatacagacggacagt 60
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Db     191 ATGAGAGTGATTCGCGTGGGTACCCGCAAGAGCCAGCTTGCTCGCATACAGACGGACAGT 250

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Db     251 GTGGTGGCAACATTGAAAGCCTCGTACCCTGGCCTGCAGTTTGAAATCATTGCTATGTCC 310

Qy     121 accacaggggacaagattcttgatactgcactctctaagattggagagaaaagcctgttt 180
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Db     311 ACCACAGGGGACAAGATTCTTGATACTGCACTCTCTAAGATTGGAGAGAAAAGCCTGTTT 370

Qy     181 accaaggagcttgaacatgccctggagaagaatgaagtggacctggttgttcactccttg 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     371 ACCAAGGAGCTTGAACATGCCCTGGAGAAGAATGAAGTGGACCTGGTTGTTCACTCCTTG 430

Qy     241 aaggacctgcccactgtgcttcctcctggcttcaccatcggagccatctgcaagcgggaa 300
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Db     431 AAGGACCTGCCCACTGTGCTTCCTCCTGGCTTCACCATCGGAGCCATCTGCAAGCGGGAA 490

Qy     301 aaccctcatgatgctgttgtctttcacccaaaatttgttgggaagaccctagaaaccctg 360
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Db     491 AACCCTCATGATGCTGTTGTCTTTCACCCAAAATTTGTTGGGAAGACCCTAGAAACCCTG 550

Qy     361 ccagagaagagtgtggtgggaaccagctccctgcgaagagcagcccagctgcagagaaag 420
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Db     551 CCAGAGAAGAGTGTGGTGGGAACCAGCTCCCTGCGAAGAGCAGCCCAGCTGCAGAGAAAG 610

Qy     421 ttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttcggaagctg 480
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Db     611 TTCCCGCATCTGGAGTTCAGGAGTATTCGGGGAAACCTCAACACCCGGCTTCGGAAGCTG 670

Qy     481 gacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatg-gg 539
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Db     671 GACGAGCAGCAGGAGTTCAGTGCCATCATCCTGGCAACAGCTGGCCTGCAGCGCATGTGG 730

Qy     540 ctggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctgtgggcca 599
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Db     731 CTGGCACAACCGGGTGGGGCAGATCCTGCACCCTGAGGAATGCATGTATGCTGTGGGCCA 790

Qy     600 gggggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgt 659
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Db     791 GGGGG-CTTGGGCGTGGAAGTGCGAGCCAAGGACCAGGACATCTTGGATCTGGTGGGTGT 849

Qy     660 gctgcacgatcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacct 719
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Db     850 GCTGCACGATCCCGAGACTCTGCTTCGCTGCATCGCTGAAAGGGCYTTCCTGAG--CACC 907

Qy     720 ggaaggaggctgcagtgtgc 739
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Db     908 TGGAAGAGGCTGCAGTGTGC 927
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RESULT   7
AL579416/c
LOCUS       AL579416      838 bp    mRNA            EST       16-FEB-2001
DEFINITION  AL579416 LTI_FL012_TC1 Homo sapiens cDNA clone CS0DH004YP13 3 prime
            , mRNA sequence.
ACCESSION   AL579416
VERSION     AL579416.1  GI:12944439
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 838)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
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                     /lab_host="DH10B"
                     /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-stranded cDNA was digested with Not I and cloned
                     into the Not I and Eco RV sites of the pCMVSPORT 6 vector.
                     Library was constructed by Life Technologies. Contact :
                     Feng Liang Life Technologies, a division of Invitrogen
                     9800 Medical Center Drive Rockville, Maryland 20850, USA
                     Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      160 a    243 c    225 g    189 t     21 others
ORIGIN
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Db     838 AAACCCTCATGATGCTKTTGTCTTTCACCCAAAATTTGTT-GGAAGACCCTAGAAACCCT 780

Qy     360 gccagagaagagtgtggtgggaaccagctccctgcgaagagcagcccagctgcagagaaa 419
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Db    779 GCCAGAGAAGAGTGTGGTGGGAACCAGCTCCCTGCGAAGAGCAGCCCAGCTGCAGAGAAA 720

Qy    420 gttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttcggaagct 479
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Db    719 GTTCCCGCATCTGGAGTTCAGGAGTATTCGGGGAAACCTCAACACCCGGCTTCGGAAGCT 660

Qy    480 ggacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatggg 539
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Db    659 GGACGAGCAGCAGGAGTTCAGTGCCATCATCCTGGCAACAGCTGGCCTGCAGCGCATGGG 600

Qy    540 ctggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctgtgggcca 599
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    599 CTGGCACAACCGGGTGGGGCAGATCCTGCACCCTGAGGAATGCATGTATGCTGTGGGCCA 540

Qy    600 ggggggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgt 659
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Qy    660 gctgcacgatcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacct 719
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Db    479 GCTGCACGATCCCGAGACTCT-CTTCGCTGCATCGCTGAAAGGGCCTTCCTGAGGCACCT 421

Qy    720 ggaaggaggctgcagtgtgccagtagccgtgcatacagctatgaaggatgggcaactgta 779
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Db    360 CCTCACTGGAGGASTCTGGAGTCTAGACSGCCCAGATMGCATACAAGAGMCCATGCAGGC 301

Qy    840 taccatccatgtccctgcccagcatgaagatggccctgaggatgacccacagttggtagg 899
          ||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||:|
Db    300 TACCATCCATGTCCCTSCCCAGCATGAAGATGGCCCTGAGGATGACCCACAGTTGGTASG 241

Qy    900 catcactgctcgtaacattccacgagggccccagttggctgcccagaacttgggcatcag 959
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Db    240 CATCACYGCYCGTMACATTCCACGAGGGCCCCAGTTGGCTGCCCARAACTTGGGCATCTM 181

Qy    960 cctggccaacttgttgctgagcaaaggagccaaaaacatcctggatgttgcacggcaatt 1019
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Db    180 CCTGGCCAAMAARTAGCTGAAMAAAGGAAMAAAAAACATCCTGGATGTDGCACGGCAGCT 121

Qy   1020 gaacgatgcccattaa 1035
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Db    120 TAACGATGCCSATTRA 105


RESULT   8
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LOCUS       BE547860      804 bp    mRNA            EST       09-AUG-2000
DEFINITION  601074758F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3460575 5',
            mRNA sequence.
ACCESSION   BE547860
VERSION     BE547860.1  GI:9776505
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 804)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Incyte Genomics, Inc.
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM8455  row: d  column: 16
            High quality sequence stop: 670.
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                      /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
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                      Average insert size 1.4 kb. Library prepared by Life
                      Technologies."
BASE COUNT       171 a    226 c    235 g    172 t
ORIGIN


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Qy     68 caacattgaaagcctcgtaccctggcctgcagtttgaaatcattgctatgtccaccacag 127
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CAACATTGAAAGCCTCGTACCCTGGCCTGCAGTTTGAAATCATTGCTATGTCCACCACAG 120

Qy    128 gggacaagattcttgatactgcactctctaagattggagagaaaagcctgtttaccaagg 187
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Db    121 GGGACAAGATTCTTGATACTGCACTCTCTAAGATTGGAGAGAAAAGCCTGTTTACCAAGG 180

Qy    188 agcttgaacatgccctggagaagaatgaagtggacctggttgttcactccttgaaggacc 247
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AGCTTGAACATGCCCTGGAGAAGAATGAAGTGGACCTGGTTGTTCACTCCTTGAAGGACC 240

Qy    248 tgcccactgtgcttcctcctggcttcaccatcggagccatctgcaagcgggaaaaccctc 307
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TGCCCACTGTGCTTCCTCCTGGCTTCACCATCGGAGCCATCTGCAAGCGGGAAAACCCTC 300

Qy    308 atgatgctgttgtctttcacccaaaatttgttgggaagaccctagaaaccctgccagaga 367
          |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db    301 ATGATGCTGTTGTCTTTCACCCAAAATTCGTTGGGAAGACCCTAGAAACCCTGCCAGAGA 360

Qy    368 agagtgtggtgggaaccagctccctgcgaagagcagcccagctgcagagaaagttcccgc 427
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AGAGTGTGGTGGGAACCAGCTCCCTGCGAAGAGCAGCCCAGCTGCAGAGAAAGTTCCCGC 420

Qy    428 atctggagttcaggagtattcggggaaacctcaacacccggcttcggaagctggacgagc 487
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Db    421 ATCTGGAGTTCAGGAGTATTCGGGGAAACCTCAACACCCGGCTTCGGAAGCTGGACGAGC 480

Qy    488 agcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatgggctggcaca 547
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Db    481 AGCAGGAGTTCAGTGCCATCATCCTGGCAACAGCTGGCCTGCAGCGCATGGGCTGGCACA 540

Qy    548 accgggttgggcagatcctgcaccctgaggaatgcatgtatgctgtgggccaggggggcct 607
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Qy    608 tgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtgctgcacg 667
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Qy    668 atcccgagactctg--cttcgctgcatcgctga--aagggccttcctgaggcacctggaa 723
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Db    661 ATCCCGAGACTCTGGCTTCGCTTGCATCGCTTACTAGGGGCTTTCCTGAGGCACCTGGAA 720

Qy    724 -ggaggctgcagtgt-gccagtagccgtgcatacagctatgaaggatgggcaactgtacc 781
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Db    721 CCGATGCTGCGTTGTGGCCCGTATCCGTTCCTTCCGCCTCTCCCGCTGCGTCCCTGGTCC 780
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Qy    782 tgactggag 790
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RESULT  9
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LOCUS       AL520284      919 bp    mRNA            EST       13-FEB-2001
DEFINITION  AL520284 LTI_NFL004_NBC2 Homo sapiens cDNA clone CS0DB006YG07 3
            prime, mRNA sequence.
ACCESSION   AL520284
VERSION     AL520284.1  GI:12783777
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 919)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .919
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                     /db_xref="taxon:9606"
                     /clone="CS0DB006YG07"
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                     /sex="male"
                     /tissue_type="neuroblastoma cells"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector.  Library was normalized. Library was constructed
                     by Life Technologies.  Contact : Feng Liang Life
                     Technologies, a division of Invitrogen 9800 Medical Center
                     Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
                     8371 Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      191 a    276 c    248 g    202 t      2 others
ORIGIN


  Query Match             63.7%;  Score 659.2;  DB 105;  Length 919;
  Best Local Similarity   98.7%;  Pred. No. 1.5e-165;
  Matches  705;  Conservative    1;  Mismatches    4;  Indels    4;  Gaps    4;

Qy    322 tttcacccaaaatttgttgggaagaccctagaaaccctgccagagaagagtgtggtggga 381
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Db    918 YTTCACCCAAAATTTGTT-GGAAGACCCTAGAAACCCTGCCAGAGAAGAGTGTGGT-GGA 861

Qy    382 accagctccctgcgaagagcagcccagctgcagagaaagttcccgcatctggagttcagg 441
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Db    860 ACCAGCTCCCTGCGAAGAGCAGCCCAGCTGCAGAGAAAGTTCCCGCATCTGGAGTTCAGG 801

Qy    442 agtattcggggaaacctcaacacccggcttcggaagctggacgagcagcaggagttcagt 501
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Db    800 AGTATTC-GGGAAACCTCAACACCCGGCTTCGGAAGCTGGACGAGCAGCAGGAGTTCAGT 742

Qy    502 gccatcatcctggcaacagctggcctgcagcgcatgggctggcacaaccgggttgggcag 561
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Db    741 GCCATCATCCTGGCAACAGCTGGCCTGCAGCGCATGGGCTGGCACAACCGGGTGGGGCAG 682

Qy    562 atcctgcaccctgaggaatgcatgtatgctgtgggccaggggccttgggcgtggaagtg 621
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    681 ATCCTGCACCCTGAGGAATGCATGTATGCTGTGGGCCAGGGGGCCTTGGGCGTGGAAGTG 622

Qy    622 cgagccaaggaccaggacatcttggatctggtgggtgtgctgcacgatcccgagactctg 681
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    621 CGAGCCAAGGACCAGGACATCTTGGATCTGGTGGGTGTGCTGCACGATCCCGAGACTCT- 561

Qy    682 cttcgctgcatcgctgaaagggccttcctgaggcacctggaaggaggctgcagtgtgcca 741
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    562 CTTCGCTGCATCGCTGAAAGGGCCTTCCTGAGGCACCTGGAAGGAGGCTGCAGTGTGCCA 503

Qy    742 gtagccgtgcatacagctatgaaggatgggcaactgtacctgactggaggagtctggagt 801
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    502 GTAGCCGTGCATACAGCTATGAAGGATGGGCAACTGTACCTGACTGGAGGAGTCTGGAGT 443

Qy    802 ctagacggctcagatagcatacaagagaccatgcaggctaccatccatgtccctgcccag 861
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    442 CTAGACGGCTCAGATAGCATACAAGAGACCATGCAGGCTACCATCCATGTCCCTGCCCAG 383

Qy    862 catgaagatggccctgaggatgacccacagttggtaggcatcactgctcgtaacattcca 921
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    382 CATGAAGATGGCCCTGAGGATGACCCACAGTTGGTAGGCATCACTGCTCGTAACATTCCA 323

Qy    922 cgagggccccagttggctgcccagaacttgggcatcagcctggccaacttgttgctgagc 981
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    322 CGAGGGCCCCAGTTGGCTGCCCAGAACTTGGGCATCAGCCTGGCCAACTTGTTGCTGAGC 263

Qy    982 aaaggagccaaaaacatcctggatgttgcacggcaattgaacgatgcccattaa 1035
          |||||||||||||||||||||||||||||||  | ||||||||||||||||
Db    262 AAAGGAGCCAAAAACATCCTGGATGTTGCACGGCAGCTTAACGATGCCCATTAA 209


RESULT  10
BF035760
LOCUS       BF035760      801 bp    mRNA            EST       20-OCT-2000
DEFINITION  601458755F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862453 5',
            mRNA sequence.
ACCESSION   BF035760
VERSION     BF035760.1  GI:10743500
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 801)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9600  row: m  column: 14
            High quality sequence stop: 678.
FEATURES             Location/Qualifiers
     source          1. .801
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3862453"
                     /clone_lib="NIH_MGC_66"
                     /tissue_type="adenocarcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.8 kb.   Library constructed by Life
                     Technologies.  "
BASE COUNT      192 a    212 c    241 g    156 t
ORIGIN


  Query Match             62.8%;  Score 650.4;  DB 143;  Length 801;
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  Best Local Similarity   99.7%;  Pred. No. 3.3e-163;
  Matches  662;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy    180 taccaaggagcttgaacatgccctggagaagaatgaa-gtggacctggttgttcactcct 238
          ||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db      1 TACCAAGGAGCTTGAACATGCCCTGGAGAAGAATGAATGTGGACCTGGTTGTTCACTCCT 60

Qy    239 tgaaggacctgcccactgtgcttcctcctggcttcaccatcggagccatctgcaagcggg 298
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGAAGGACCTGCCCACTGTGCTTCCTCCTGGCTTCACCATCGGAGCCATCTGCAAGCGGG 120

Qy    299 aaaaccctcatgatgctgttgtctttcacccaaaatttgttgggaagaccctagaaaccc 358
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAACCCTCATGATGCTGTTGTCTTTCACCCAAAATTTGTTGGGAAGACCCTAGAAACCC 180

Qy    359 tgccagagaagagtgtggtgggaaccagctccctgcgaagagcagcccagctgcagagaa 418
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TGCCAGAGAAGAGTGTGGTGGGAACCAGCTCCCTGCGAAGAGCAGCCCAGCTGCAGAGAA 240

Qy    419 agttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttcggaagc 478
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AGTTCCCGCATCTGGAGTTCAGGAGTATTCGGGGAAACCTCAACACCCGGCTTCGGAAGC 300

Qy    479 tggacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatgg 538
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGGACGAGCAGCAGGAGTTCAGTGCCATCATCCTGGCAACAGCTGGCCTGCAGCGCATGG 360

Qy    539 gctggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctgtgggcc 598
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTGGCACAACCGGGTGGGGCAGATCCTGCACCCTGAGGAATGCATGTATGCTGTGGGCC 420

Qy    599 agggggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtg 658
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AGGGGGCCTTGGGCGTGGAAGTGCGAGCCAAGGACCAGGACATCTTGGATCTGGTGGGTG 480

Qy    659 tgctgcacgatcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacc 718
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TGCTGCACGATCCCGAGACTCTGCTTCGCTGCATCGCTGAAAGGGCCTTCCTGAGGCACC 540

Qy    719 tggaaggaggctgcagtgtgccagtagccgtgcatacagctatgaaggatgggcaactgt 778
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGGAAGGAGGCTGCAGTGTGCCAGTAGCCGTGCATACAGCTATGAAGGATGGGCAACTGT 600

Qy    779 acctgactggaggagtctggagtctagacggctcagatagcatacaagagaccatgcagg 838
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 ACCTGACTGGAGGAGTCTGGAGTCTAGACGGCTCAGATAGCATACAAGAGACCATGCAGG 660

Qy    839 ctac 842
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Db    661 CTAC 664
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RESULT 11
BE561357
LOCUS       BE561357     1136 bp    mRNA            EST       15-AUG-2000
DEFINITION  601344923F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677764 5',
            mRNA sequence.
ACCESSION   BE561357
VERSION     BE561357.1  GI:9805077
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1136)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM353  row: n  column: 05
            High quality sequence stop: 714.
FEATURES              Location/Qualifiers
     source           1. .1136
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:3677764"
                      /clone_lib="NIH_MGC_8"
                      /tissue_type="Burkitt lymphoma"
                      /lab_host="DH10B (phage-resistant)"
                      /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                      EcoRI; cDNA made by oligo-dT priming.  Directionally
                      cloned into EcoRI/XhoI sites using the following 5'
                      adaptor: GGCACGAG(G).  Size-selected >500bp for average
                      insert size 1.8kb.  Library constructed by Ling Hong in
                      the laboratory of Gerald M. Rubin (University of
                      California, Berkeley) using  ZAP-cDNA synthesis kit
                      (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      280 a    298 c    341 g    217 t
ORIGIN
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  Query Match             62.7%;  Score 649.2;  DB 137;  Length 1136;
  Best Local Similarity   94.8%;  Pred. No. 7.6e-163;
  Matches  713;  Conservative    0;  Mismatches   13;  Indels   26;  Gaps    3;

Qy      1 atgagagtgattcgcgtgggtacccgcaagagccagcttgctcgcatacagacggacagt 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     58 ATGAGAGTGATTCGCGTGGGTACCCGCAAGAGCCAGCTTGCTCGCATACAGACGGACAGT 117

Qy     61 gtggtggcaacattgaaagcctcgtaccctggcctgcagtttgaaatcattgctatgtcc 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    118 GTGGTGGCAACATTGAAAGCCTCGTACCCTGGCCTGCAGTTTGAAATCATTGCTATGTCC 177

Qy    121 accacaggggacaagattcttgatactgcactctctaagattggagagaaaagcctgttt 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    178 ACCACAGGGGACAAGATTCTTGATACTGCACTCTCTAAGATTGGAGAGAAAAGCCTGTTT 237

Qy    181 accaaggagcttgaacatgccctggagaagaatgaagtggacctggttgttcactccttg 240
          ||||||||||||||||||||||||||||||||||||
Db    238 ACCAAGGAGCTTGAACATGCCCTGGAGAAGAATGAAGT---------------------- 275

Qy    241 aaggacctgcccactgtgcttcctcctggcttcaccatcggagccatctgcaagcgggaa 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    276 --GGACCTGCCCACTGTGCTTCCTCCTGGCTTCACCATCGGAGCCATCTGCAAGCGGGAA 333

Qy    301 aaccctcatgatgctgttgtctttcacccaaaatttgttgggaagaccctagaaaccctg 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    334 AACCCTCATGATGCTGTTGTCTTTCACCCAAAATTTGTTGGGAAGACCCTAGAAACCCTG 393

Qy    361 ccagagaagagtgtggtgggaaccagctccctgcgaagagcagcccagctgcagagaaag 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    394 CCAGAGAAGAGTGTGGTGGGAACCAGCTCCCTGCGAAGAGCAGCCCAGCTGCAGAGAAAG 453

Qy    421 ttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttcggaagctg 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    454 TTCCCGCATCTGGAGTTCAGGAGTATTCGGGGAAACCTCAACACCCGGCTTCGGAAGCTG 513

Qy    481 gacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatgggc 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    514 GACGAGCAGCAGGAGTTCAGTGCCATCATCCTGGCAACAGCTGGCCTGCAGCGCATGGGC 573

Qy    541 tggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgc-tgtgggcca 599
          |||||||||||||| ||||||||||||||||||||||||||||||||| ||||||||| |||
Db    574 TGGCACAACCGGGTGGGGCAGATCCTGCACCCTGAGGAATGCATGTATGCTTGTGGGCCA 633

Qy    600 gggggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgt 659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    634 GGGGGCCTTGGGCGTGGAAGTGCGAGCCAAGGACCAGGACATCTTGGATCTGGTGGGTGT 693
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Qy    660 gctgcacgatcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacct 719
          ||||||||||||||||||||||||||| || |||||||||||||| | |   ||||||
Db    694 GCTGCACGATCCCGAGACTCTGCTTCGGTGGATCGCTGAAAGGGCTTCCTGAAGGCACTG 753

Qy    720 ggaagga-ggctgcagtgtgccagtagccgtg 750
          ||||||| || |||||||||||||| ||| |
Db    754 GGAAGGAGGGTTGCAGTGTGCCAGTACCCGGG 785


RESULT 12
BG469642
LOCUS       BG469642      835 bp    mRNA            EST       21-MAR-2001
DEFINITION  602533692F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4661422 5',
            mRNA sequence.
ACCESSION   BG469642
VERSION     BG469642.1  GI:13401917
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 835)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: NIH Intramural Sequencing Center
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1460  row: g  column: 23
            High quality sequence stop: 824.
FEATURES             Location/Qualifiers
     source          1. .835
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4661422"
                     /clone_lib="NIH_MGC_15"
                     /tissue_type="adenocarcinoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)"
BASE COUNT      194 a    229 c    250 g    162 t
ORIGIN


  Query Match             62.5%;  Score 646.4;  DB 154;  Length 835;
  Best Local Similarity   99.6%;  Pred. No. 4e-162;
  Matches  669;  Conservative    0;  Mismatches    1;  Indels    2;  Gaps    2;

Qy      1 atgagagtgattcgcgtgggtacccgcaagagccagcttgctcgcatacagacggacagt 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    163 ATGAGAGTGATTCGCGTGGGTACCCGCAAGAGCCAGCTTGCTCGCATACAGACGGACAGT 222

Qy     61 gtggtggcaacattgaaagcctcgtaccctggcctgcagtttgaaatcattgctatgtcc 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    223 GTGGTGGCAACATTGAAAGCCTCGTACCCTGGCCTGCAGTTTGAAATCATTGCTATGTCC 282

Qy    121 accacaggggacaagattcttgatactgcactctctaagattggagagaaaagcctgttt 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    283 ACCACAGGGGACAAGATTCTTGATACTGCACTCTCTAAGATTGGAGAGAAAAGCCTGTTT 342

Qy    181 accaaggagcttgaacatgccctggagaagaatgaagtggacctggttgttcactccttg 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    343 ACCAAGGAGCTTGAACATGCCCTGGAGAAGAATGAAGTGGACCTGGTTGTTCACTCCTTG 402

Qy    241 aaggacctgcccactgtgcttcctcctggcttcaccatcggagccatctgcaagcgggaa 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    403 AAGGACCTGCCCACTGTGCTTCCTCCTGGCTTCACCATCGGAGCCATCTGCAAGCGGGAA 462

Qy    301 aaccctcatgatgctgttgtctttcacccaaaatttgttgggaagaccctagaaaccctg 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    463 AACCCTCATGATGCTGTTGTCTTTCACCCAAAATTTGTTGGGAAGACCCTAGAAACCCTG 522

Qy    361 ccagagaagagtgtggtgggaaccagctccctgcgaagagcagcccagctgcagagaaag 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    523 CCAGAGAAGAGTGTGGTGGGAACCAGCTCCCTGCGAAGAGCAGCCCAGCTGCAGAGAAAG 582

Qy    421 ttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttcggaagctg 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    583 TTCCCGCATCTGGAGTTCAGGAGTATTCGGGGAAACCTCAACACCCGGCTTCGGAAGCTG 642

Qy    481 gacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatgggc 540
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Db    643 GACGAGCAGCAGGAGTTCAGTGCCATCATCCTGGCAACAGCTGGCCTGCAGCGCATGGGC 702

Qy    541 tggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctgtgggccag 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    703 TGGCACAACCGGGTTGGGCAGATCCTGCACCCTGAGGAATGCATGTATGCTGTGGGCCAG 762

Qy    601 ggggccttgggcg-tggaagtgcgagccaaggaccaggacatcttggatctggtgggtgt 659
          |||||||||||| |||||||||||||||||||||||||||||||||||||||| ||||||||
Db    763 GGGGCCTTGGGCGTTGGAAGTGCGAGCCAAGGACCAGGACATCTTGGATCT-GTGGGTGT 821

Qy    660 gctgcacgatcc 671
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Db    822 GCTGAACGATCC 833


RESULT 13
AL520223
LOCUS       AL520223      908 bp    mRNA            EST       13-FEB-2001
DEFINITION  AL520223 LTI_NFL004_NBC2 Homo sapiens cDNA clone CS0DB006YI03 5
            prime, mRNA sequence.
ACCESSION   AL520223
VERSION     AL520223.1  GI:12783716
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 908)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .908
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DB006YI03"
                     /clone_lib="LTI_NFL004_NBC2"
                     /sex="male"
                     /tissue_type="neuroblastoma cells"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector.  Library was normalized. Library was constructed
                     by Life Technologies.  Contact : Feng Liang Life
                     Technologies, a division of Invitrogen 9800 Medical Center
                     Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
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                    8371 Email : fliang@lifetech.com URL :
                    http://fulllength.invitrogen.com"
BASE COUNT      208 a    245 c    269 g    183 t      3 others
ORIGIN


  Query Match             61.4%;  Score 635.6;  DB 105;  Length 908;
  Best Local Similarity   99.2%;  Pred. No. 3.1e-159;
  Matches  657;  Conservative    2;  Mismatches    1;  Indels    2;  Gaps    2;

Qy       1 atgagagtgattcgcgtgggtacccgcaagagccagcttgctcgcatacagacggacagt 60
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Db     249 ATGAGAGTGATTCGCGTGGGTACCCGCAAGAGCCAGCTTGCTCGCATACAGACGGACAGT 308

Qy      61 gtggtggcaacattgaaagcctcgtaccctggcctgcagtttgaaatcattgctatgtcc 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     309 GTGGTGGCAACATTGAAAGCCTCGTACCCTGGCCTGCAGTTTGAAATCATTGCTATGTCC 368

Qy     121 accacaggggacaagattcttgatactgcactctctaagattggagagaaaagcctgttt 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     369 ACCACAGGGGACAAGATTCTTGATACTGCACTCTCTAAGATTGGAGAGAAAAGCCTGTTT 428

Qy     181 accaaggagcttgaacatgccctggagaagaatgaagtggacctggttgttcactccttg 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     429 ACCAAGGAGCTTGAACATGCCCTGGAGAAGAATGAAGTGGACCTGGTTGTTCACTCCTTG 488

Qy     241 aaggacctgcccactgtgcttcctcctggcttcaccatcggagccatctgcaagcgggaa 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     489 AAGGACCTGCCCACTGTGCTTCCTCCTGGCTTCACCATCGGAGCCATCTGCAAGCGGGAA 548

Qy     301 aaccctcatgatgctgttgtctttcacccaaaatttgttgggaagaccctagaaaccctg 360
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Db     549 AACCCTCATGATGCTGTTGTCTTTCACCCAAAATTTGTTGGGAAGACCCTAGAAACCCTG 608

Qy     361 ccagagaagagtgtggtgggaaccagctccctgcgaagagcagcccagctgcagagaaag 420
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Qy     481 gacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatgggc 540
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Db     727 GACGAGCAGCAGGAGTTCAGTGCCATCATCCTGGCAACAGCTGGCCTGCAGCGCATGGGC 786

Qy     541 tggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctgtgggccag 600
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Db     787 TGGCACAACCGGGTGGGGCAGATCCTGCACCCTGAGGAATGCATGTATGCTGTGGGCCAG 846

Qy     601 ggggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtg 660
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Db     847 GGGGCCTTGGGCGTGGAAGTGCGAGCCAAGGACCAGGACATCTTGGATCTGGTGGGTGTG 906

Qy     661 ct 662
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Db     907 CK 908


RESULT  14
AL561775/c
LOCUS       AL561775      941 bp    mRNA            EST       16-FEB-2001
DEFINITION  AL561775 LTI_NFL004_NBC2 Homo sapiens cDNA clone CS0DB004YB23 3
            prime, mRNA sequence.
ACCESSION   AL561775
VERSION     AL561775.1  GI:12909540
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 941)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .941
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DB004YB23"
                     /clone_lib="LTI_NFL004_NBC2"
                     /sex="male"
                     /tissue_type="neuroblastoma cells"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector.  Library was normalized. Library was constructed
                     by Life Technologies.  Contact : Feng Liang Life
                     Technologies, a division of Invitrogen 9800 Medical Center
                     Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
                     8371 Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      300 a    243 c    208 g    173 t     17 others
ORIGIN


  Query Match             60.8%;  Score 628.8;  DB 106;  Length 941;
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  Matches  663;  Conservative    2;  Mismatches    4;  Indels    3;  Gaps    3;

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Db     941 GAGAAGAGTGTGGTGGGAACCAGCTCCCTGCGAAGA-CMGCCCAGCTGCAGAGAAAGTTC 883

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Db     882 CCGCATCTGGAGTTCAGGAGTATTC-GGGAAACCTCAACACCCGGCTTCGGAAGCTGGAC 824

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Db     823 GAGCAGCAGGAGTTCAGTGCCATCATCCTGGCAACAGCTGGCCTGCAGCGCATGGGCTGG 764

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Qy     604 gccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtgctg 663
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Db     643 CACGATCCCGAGACTCT-STTCGCTGCATCGCTGAAAGGGCCTTCCTGAGGCACCTGGAA 585

Qy     724 ggaggctgcagtgtgccagtagccgtgcatacagctatgaaggatgggcaactgtacctg 783
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Db     584 GGAGGCTGCAGTGTGCCAGTAGCCGTGCATACAGCTATGAAGGATGGGCAACTGTACCTG 525

Qy     784 actggaggagtctggagtctagacggctcagatagcatacaagagaccatgcaggctacc 843
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     844 atccatgtccctgcccagcatgaagatggccctgaggatgacccacagttggtaggcatc 903
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Qy     904 actgctcgtaacattccacgagggccccagttggctgcccagaacttgggcatcagcctg 963
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RESULT 15
AU132868
LOCUS       AU132868      812 bp    mRNA            EST       24-OCT-2000
DEFINITION  AU132868 NT2RP4 Homo sapiens cDNA clone NT2RP4000750 5', mRNA
            sequence.
ACCESSION   AU132868
VERSION     AU132868.1  GI:10993407
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 812)
  AUTHORS   Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Yamamoto,J.,
            Nishikawa,T., Nakamura,Y., Nagai,T., Sugano,S., Masuho,Y. and
            Isogai,T.
  TITLE     HRI human cDNA project (Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y.,
            Saito,K., Yamamoto,J., Nishikawa,T., Nakamura,Y., Nagai,T., Sugano
            ,S., Masuho,Y., Isogai,T.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Takao Isogai
            Genomics Laboratory
            Helix Research Institute
            1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            Tel: 81-438-52-3951
            Fax: 81-438-52-3952
            Email: genomics@hri.co.jp
            HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
            Research Institute; cDNA library construction: Department of
            Virology, Institute of Medical Science, University of Tokyo, and
            Helix Research Institute.
FEATURES             Location/Qualifiers
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                     /clone_lib="NT2RP4"
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                     /cell_line="NT2"
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                     cells after 2-weeks retinoic acid (RA) induction"
BASE COUNT      193 a    226 c    241 g    152 t
ORIGIN


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  Best Local Similarity  99.2%;  Pred. No. 1.9e-152;
  Matches  634;  Conservative    0;  Mismatches    3;  Indels    2;  Gaps    2;

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Db    175 ATGAGAGTGATTCGCGTGGGTACCCGCAAGAGCCAGCTTGCTCGCATACAGACGGACAGT 234

Qy     61 gtggtggcaacattgaaagcctcgtaccctggcctgcagtttgaaatcattgctatgtcc 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    235 GTGGTGGCAACATTGAAAGCCTCGTACCCTGGCCTGCAGTTTGAAATCATTGCTATGTCC 294

Qy    121 accacaggggacaagattcttgatactgcactctctaagattggagagaaaagcctgttt 180
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Db    295 ACCACAGGGGACAAGATTCTTGATACTGCACTCTCTAAGATTGGAGAGAAAAGCCTGTTT 354

Qy    181 accaaggagcttgaacatgccctggagaagaatgaagtggacctggttgttcactccttg 240
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Db    355 ACCAAGGAGCTTGAACATGCCCTGGAGAAGAATGAAGTGGACCTGGTTGTTCACTCCTTG 414

Qy    241 aaggacctgcccactgtgcttcctcctggcttcaccatcggagccatctgcaagcgggaa 300
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Db    415 AAGGACCTGCCCACTGTGCTTCCTCCTGACTTCACCATCGGAGCCATCTGCAAGCGGGAA 474

Qy    301 aaccctcatgatgctgttgtctttcacccaaaatttgttgggaagaccctagaaaccctg 360
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Db    475 AACCCTCATGATGCTGTTGTCTTTCACCCAAAATTTGTTGGGAAGACCCTAGAAACCCTG 534

Qy    361 ccagagaagagtgtggtgggaaccagctccctgcgaagagcagcccagctgcagagaaag 420
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Db    535 CCAGAGAAGAGTGTGGTGGGAACCAGCTCCCTGCGAAGAGCAGCCCAGCTGCAGAGAAAG 594

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Db    655 GACGAGCAGCAGGAGTTCAGTGCCATCATCCTGGCAACAGCTGGCCTGCAGCGCATGGGC 714

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GenCore version 4.5

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Title: US-09-601-138-1
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Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	36.2	3.5	290	1	US-08-030-731A-41	Sequence 41, Appl
c	3	36.2	3.5	290	1	US-08-030-731A-42	Sequence 42, Appl
	4	36.2	3.5	304	1	US-07-696-551B-12	Sequence 12, Appl
c	5	35.6	3.4	7218	1	US-08-232-463-14	Sequence 14, Appl
c	6	34.8	3.4	1889	2	US-08-946-241B-1	Sequence 1, Appli
c	7	34.8	3.4	1889	2	US-08-946-241B-8	Sequence 8, Appli
c	8	34.8	3.4	1889	3	US-09-309-053-1	Sequence 1, Appli
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	10	34.4	3.3	2502	1	US-08-073-384C-7	Sequence 7, Appli
	11	34.4	3.3	2502	1	US-08-254-359A-7	Sequence 7, Appli
	12	34.4	3.3	2502	1	US-08-483-043-7	Sequence 7, Appli
	13	34.4	3.3	2502	1	US-08-481-238-7	Sequence 7, Appli
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	15	34.4	3.3	2502	2	US-08-484-956-7	Sequence 7, Appli
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	17	34.4	3.3	2502	2	US-08-599-491-7	Sequence 7, Appli
	18	34.4	3.3	2502	2	US-08-756-386-7	Sequence 7, Appli
	19	34.4	3.3	2502	2	US-08-823-516-7	Sequence 7, Appli
	20	34.4	3.3	2502	3	US-08-682-853A-7	Sequence 7, Appli
	21	34.4	3.3	2502	3	US-08-759-038-7	Sequence 7, Appli
	22	34.4	3.3	2502	3	US-08-758-314-7	Sequence 7, Appli
	23	34.2	3.3	510	1	US-07-918-953-7	Sequence 7, Appli
	24	34.2	3.3	510	1	US-08-081-661-7	Sequence 7, Appli
	25	34.2	3.3	729	4	US-09-140-804-10	Sequence 10, Appl
	26	34.2	3.3	2793	1	US-08-209-747-1	Sequence 1, Appli
	27	34.2	3.3	2793	1	US-08-458-298-1	Sequence 1, Appli
	28	33.6	3.2	2121	4	US-09-358-683-1	Sequence 1, Appli
	29	33.6	3.2	2276	1	US-08-202-389-11	Sequence 11, Appl
	30	33.6	3.2	2394	4	US-08-797-358B-1	Sequence 1, Appli
	31	33.6	3.2	2790	1	US-08-018-129-4	Sequence 4, Appli
	32	33.6	3.2	2790	2	US-08-448-250-4	Sequence 4, Appli
	33	33.4	3.2	359	3	US-08-589-028-3	Sequence 3, Appli
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	35	33.4	3.2	359	4	US-08-785-271-3	Sequence 3, Appli
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	39	33.4	3.2	44377	2	US-08-804-198-1	Sequence 1, Appli
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	41	33	3.2	281	1	US-07-764-655D-12	Sequence 12, Appl
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	43	33	3.2	281	6	5514646-1	Patent No. 5514646
	44	33	3.2	3579	1	US-08-674-168-15	Sequence 15, Appl
	45	33	3.2	3579	3	US-08-985-908-18	Sequence 18, Appl

ALIGNMENTS

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RESULT 1
US-08-599-480-3/c
; Sequence 3, Application US/08599480
; Patent No. 5753459
;  GENERAL INFORMATION:
;    APPLICANT:  Blanco, David R.
;    APPLICANT:  Miller, James N.
;    APPLICANT:  Lovett, Michael A.
;    APPLICANT:  Champion, Cheryl I.
;    APPLICANT:  Tempst, Paul J.
;    TITLE OF INVENTION:  NUCLEOTIDE AND AMINO ACID SEQUENCES OF A
;    TITLE OF INVENTION:  T. Pallidum RARE OUTER MEMBRANE PROTEIN
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/599,480
;      FILING DATE:  23-JAN-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Learn, June M.
;      REGISTRATION NUMBER:  31,238
;      REFERENCE/DOCKET NUMBER:  07419/018001 (CIP of 016001)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 678-5070
;      TELEFAX:  (619) 678-5099
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  729 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  TROMP2
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..726
US-08-599-480-3
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  Query Match             4.0%;  Score 41.6;  DB 1;  Length 729;
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  Matches  125;  Conservative    0;  Mismatches  139;  Indels    0;  Gaps    0;

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Qy     296 gggaaaaccctcatgatgctgttg 319
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RESULT   2
US-08-030-731A-41
; Sequence 41, Application US/08030731A
; Patent No. 5426036
;  GENERAL INFORMATION:
;    APPLICANT:  Koller, Klaus-Peter
;    APPLICANT:  Riess, Guenther Johannes
;    APPLICANT:  Uhlmann, Eugen
;    APPLICANT:  Wallmeier, Holger
;    TITLE OF INVENTION:  Processes for the Preparation of Foreign
;    TITLE OF INVENTION:  Proteins in Streptomycetes
;    NUMBER OF SEQUENCES:  48
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W., Suite 700
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/030,731A
;      FILING DATE:  12-MAR-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/189,840
;      FILING DATE:  03-MAY-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/430,622
;      FILING DATE:  01-NOV-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/687,610
;      FILING DATE:  19-APR-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/735,757
;      FILING DATE:  29-JUL-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P 37 14 866.4
;      FILING DATE:  05-MAY-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P 38 37 273.8
;      FILING DATE:  03-NOV-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P 39 27 449.7
;      FILING DATE:  19-AUG-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P 40 12 818.0
;      FILING DATE:  21-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kirschner Michael K.
;      REGISTRATION NUMBER:  34,851
;      REFERENCE/DOCKET NUMBER:  02481-0593-02000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-408-4000
;      TELEFAX:  202-408-4400
;  INFORMATION FOR SEQ ID NO:  41:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  290 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-030-731A-41


  Query Match             3.5%;  Score 36.2;  DB 1;  Length 290;
  Best Local Similarity   46.6%;  Pred. No. 0.15;
  Matches  116;  Conservative    0;  Mismatches  133;  Indels    0;  Gaps    0;

Qy     485 agcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatgggctggc 544
           | |||||   || | |  ||  | |  ||| | |      ||||  | ||  ||   |
Db      20 ACCAGCACCTGTGCGGCTCCCACCTAGTGGAAGCTCTCTACCTGGTGTGCGGGGAGCGAG 79

Qy     545 acaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctgtgggccaggggg 604
             |  |         |  |     | ||  |||| |        |   ||||| |||| ||
Db      80 GCTTCTTCTACACACCCAAGACCCGCCGGGAGGCAGAGGACCCTCAGGTGGGGCAGGTGG 139

Qy     605 ccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtgctgc 664
           ||||||  ||       | ||      || | |  |||||  |||| |||    ||||
Db     140 AGCTGGGCGGGGGCCCTGGCGCAGGCAGCCTGCAGCCCTTGGCGCTGGAGGGGTCCCTGC 199

Qy     665 acgatcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctggaag 724
           | | | ||  |   ||  |  |||  | |    |    || |||    || |||||
Db     200 AGAAGCGCGGCATCGTGGAGCAGTGCTGCACCAGCATCTGCTCCCTCTACCAGCTGGAGA 259

Qy     725 gaggctgca 733
           |||||
Db     260 ACTACTGCA 268


RESULT   3
US-08-030-731A-42/c
; Sequence 42, Application US/08030731A
;.Patent No. 5426036
;  GENERAL INFORMATION:
;    APPLICANT:  Koller, Klaus-Peter
;    APPLICANT:  Riess, Guenther Johannes
;    APPLICANT:  Uhlmann, Eugen
;    APPLICANT:  Wallmeier, Holger
;    TITLE OF INVENTION:  Processes for the Preparation of Foreign
;    TITLE OF INVENTION:  Proteins in Streptomycetes
;    NUMBER OF SEQUENCES:  48
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W., Suite 700
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/030,731A
;      FILING DATE:  12-MAR-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/189,840
;      FILING DATE:  03-MAY-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/430,622
;      FILING DATE:  01-NOV-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/687,610
;      FILING DATE:  19-APR-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/735,757
;      FILING DATE:  29-JUL-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P 37 14 866.4
;      FILING DATE:  05-MAY-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P 38 37 273.8
;      FILING DATE:  03-NOV-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P 39 27 449.7
;      FILING DATE:  19-AUG-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P 40 12 818.0
;      FILING DATE:  21-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kirschner Michael K.
;      REGISTRATION NUMBER:  34,851
;      REFERENCE/DOCKET NUMBER:  02481-0593-02000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-408-4000
;      TELEFAX:  202-408-4400
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  290 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ANTI-SENSE:  YES
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  5..290
;      OTHER INFORMATION:  /note= "Sequence ID No. 5426036 42 is
;      OTHER INFORMATION:  complementary to Sequence ID No. 5426036 41 at positions
;      OTHER INFORMATION:  5-290 of Sequence ID No. 5426036 41."
US-08-030-731A-42


  Query Match             3.5%;  Score 36.2;  DB 1;  Length 290;
  Best Local Similarity   46.6%;  Pred. No. 0.15;
  Matches  116;  Conservative    0;  Mismatches  133;  Indels    0;  Gaps    0;

Qy    485 agcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatgggctggc 544
          | |||||   || | |  ||  | |  ||| | |      ||||  | ||  ||   |
Db    275 ACCAGCACCTGTGCGGCTCCCACCTAGTGGAAGCTCTCTACCTGGTGTGCGGGGAGCGAG 216

Qy    545 acaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctgtgggccaggggg 604
            |  |          |  |      | ||  |||| |         |   ||||| |||| ||
Db    215 GCTTCTTCTACACACCCAAGACCCGCCGGGAGGCAGAGGACCCTCAGGTGGGGCAGGTGG 156

Qy    605 ccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtgctgc 664
            |||||| ||      | ||      || | |   |||||  |||| |||    ||||
Db    155 AGCTGGGCGGGGGCCCTGGCGCAGGCAGCCTGCAGCCCTTGGCGCTGGAGGGGTCCCTGC 96

Qy    665 acgatcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctggaag 724
          |  | | ||  |   ||  |  |||  | |    |   || |||    || |||||
Db     95 AGAAGCGCGGCATCGTGGAGCAGTGCTGCACCAGCATCTGCTCCCTCTACCAGCTGGAGA 36

Qy    725 gaggctgca 733


                ||||
Db     35 ACTACTGCA 27


RESULT   4
US-07-696-551B-12
; Sequence 12, Application US/07696551B
; Patent No. 5232841
;  GENERAL INFORMATION:
;    APPLICANT:  Hashimoto, Tamotsu
;    APPLICANT:  Tsujimura, Atsushi
;    APPLICANT:  Udaka, Shigezo
;    TITLE OF INVENTION:  Process for Preparing Peptide
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W., Suite 700
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  MS-DOS/PC-DOS
;      SOFTWARE:  Patentin Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/696,551B
;      FILING DATE:  19910509
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 2-122166
;      FILING DATE:  11-MAY-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 2-334575
;      FILING DATE:  30-NOV-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lawrence M. Lavin, Jr.
;      REGISTRATION NUMBER:  30,768
;      REFERENCE/DOCKET NUMBER:  2481-1070
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  304 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-696-551B-12


  Query Match             3.5%;  Score 36.2;  DB 1;  Length 304;
  Best Local Similarity   46.6%;  Pred. No. 0.15;
  Matches  116;  Conservative    0;  Mismatches  133;  Indels    0;  Gaps    0;

Qy    485 agcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatgggctggc 544
          | |||||   || | |  ||  | |  ||| | |      ||||  | ||  ||   |
Db     43 ACCAGCACCTGTGCGGCTCCCACCTAGTGGAAGCTCTCTACCTGGTGTGCGGGGAGCGAG 102

Qy    545 acaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctgtgggccaggggg 604
            |  |          |  |      | ||  |||| |         |   ||||| |||| ||
Db    103 GCTTCTTCTACACACCCAAGACCCGCCGGGAGGCAGAGGACCCTCAGGTGGGGCAGGTGG 162

Qy    605 ccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtgctgc 664
            |||||| ||      | ||      || | |   |||||  |||| |||    ||||
Db    163 AGCTGGGCGGGGGCCCTGGCGCAGGCAGCCTGCAGCCCTTGGCGCTGGAGGGGTCCCTGC 222

Qy    665 acgatcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctggaag 724
          |  | | ||  |   ||  |  |||  | |    |   || |||    || |||||
Db    223 AGAAGCGCGGCATCGTGGAGCAGTGCTGCACCAGCATCTGCTCCCTCTACCAGCTGGAGA 282
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Qy    725 gaggctgca 733
              |||||
Db    283 ACTACTGCA 291


RESULT   5
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-F1s
US-08-232-463-14


  Query Match             3.4%;  Score 35.6;  DB 1;  Length 7218;
  Best Local Similarity   3.3%;  Pred. No. 1.1;
  Matches   11;  Conservative  184;  Mismatches  143;  Indels    0;  Gaps    0;

Qy    340 gggaagaccctagaaaccctgccagagaagagtgtggtgggaaccagctccctgcgaaga 399
          :::::::    :::::    :  :::::::::: : :: :::::  ::       : :::::
Db   1386 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1327

Qy    400 gcagcccagctgcagagaaagttcccgcatctggagttcaggagtattcggggaaacctc 459
          : ::   ::  : ::::::::     : :   ::::   ::::: :   :::::::
Db   1326 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1267

Qy    460 aacacccggcttcggaagctggacgagcagcaggagttcagtgccatcatcctggcaaca 519
          :: :   ::    :::::  ::: ::: :: :::::   :: :  :  :    :: :: :
Db   1266 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1207

Qy    520 gctggcctgcagcgcatgggctggcacaaccgggttgggcagatcctgcaccctgaggaa 579
          :  ::   : :: : : :::  :: : ::  :::  ::: :::    : :    ::::::
Db   1206 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1147

Qy    580 tgcatgtatgctgtgggccaggggccttgggcgtggaagtgcgagccaaggaccaggac 639
          : : : :  : :::  ::::::  . ::: : ::::: : :::  :::::  ::::
Db   1146 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1087

Qy    640 atcttggatctggtgggtgtgctgcacgatcccgagac 677
          :    :::   :: ::: :    ||| | ||||  |||
Db   1086 RRRRRRRRRRRRRRRRRRRATCGCAAGCTCCCTCGAC 1049


RESULT   6
US-08-946-241B-1/c
; Sequence 1, Application US/08946241B
; Patent No. 5928941
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Mu-En
;    APPLICANT:  McA'Nulty, Megan M.
;    TITLE OF INVENTION:  REPRESSOR KRUPPEL-LIKE FACTOR
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/946,241B
;      FILING DATE:  07-OCT-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/030,035
;      FILING DATE:  05-NOV-1996
;      APPLICATION NUMBER:  60/027,521
;      FILING DATE:  07-OCT-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Creason, Gary L.
;      REGISTRATION NUMBER:  34,310
;      REFERENCE/DOCKET NUMBER:  05433/027001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-542-5070
;      TELEFAX:  617-542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1889 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  434...1843
US-08-946-241B-1


  Query Match             3.4%;  Score 34.8;  DB 2;  Length 1889;
  Best Local Similarity   52.8%;  Pred. No. 0.99;
  Matches   75;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;

Qy    608 tgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtgctgcacg 667
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Db   1434 TGGGGATGGAAGCCGGGAGGAAGCGGCAGGGCAGGGTGACAGTCCCTGCTGCTCAGCACT 1375

Qy    668 atcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctggaaggag 727
          | | |||| | |  |||  | |  |||  |||   | | |   ||  |||||  |
Db   1374 TCCTCAAGACCCAGGGTCGGGGTAGTCCTGCTGGGGAGCTGCCGCCCCAGGGGGAAGTCG 1315
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Qy    728 gctgcagtgtgccagtagccgt 749
          |||||   ||| || ||| |
Db   1314 TGTGCAGCCGGCCGGTGGCCAT 1293


RESULT   7
US-08-946-241B-8/c
; Sequence 8, Application US/08946241B
; Patent No. 5928941
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Mu-En
;    APPLICANT:  McA'Nulty, Megan M.
;    TITLE OF INVENTION:  REPRESSOR KRUPPEL-LIKE FACTOR
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/946,241B
;      FILING DATE:  07-OCT-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/030,035
;      FILING DATE:  05-NOV-1996
;      APPLICATION NUMBER:  60/027,521
;      FILING DATE:  07-OCT-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Creason, Gary L.
;      REGISTRATION NUMBER:  34,310
;      REFERENCE/DOCKET NUMBER:  05433/027001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-542-5070
;      TELEFAX:  617-542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1889 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  407...1843
US-08-946-241B-8


  Query Match             3.4%;  Score 34.8;  DB 2;  Length 1889;
  Best Local Similarity   52.8%;  Pred. No. 0.99;
  Matches   75;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;

Qy    608 tgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtgctgcacg 667
          ||||  ||||||   |    |||   |||| ||   ||    |   | ||  | ||||
Db   1434 TGGGGATGGAAGCCGGGAGGAAGCGGCAGGGCAGGGTGACAGTCCCTGCTGCTCAGCACT 1375

Qy    668 atcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctggaaggag 727
            | | |||| | |  |||  | |   |||   |||   | | |   ||   ||||| |
Db   1374 TCCTCAAGACCCAGGGTCGGGGTAGTCCTGCTGGGGAGCTGCCGCCCCAGGGGGAAGTCG 1315

Qy    728 gctgcagtgtgccagtagccgt 749
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Db   1314 TGTGCAGCCGGCCGGTGGCCAT 1293


RESULT   8
US-09-309-053-1/c
; Sequence 1, Application US/09309053
; Patent No. 6077933
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Mu-En
;    APPLICANT:  McA'Nulty, Megan M.
;    TITLE OF INVENTION:  REPRESSOR KRUPPEL-LIKE FACTOR
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/309,053
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/946,241
;      FILING DATE:  07-OCT-1997
;      APPLICATION NUMBER:  60/030,035
;      FILING DATE:  05-NOV-1996
;      APPLICATION NUMBER:  60/027,521
;      FILING DATE:  07-OCT-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Creason, Gary L.
;      REGISTRATION NUMBER:  34,310
;      REFERENCE/DOCKET NUMBER:  05433/027001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-542-5070
;      TELEFAX:  617-542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1889 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  434...1843
US-09-309-053-1


  Query Match             3.4%;  Score 34.8;  DB 3;  Length 1889;
  Best Local Similarity   52.8%;  Pred. No. 0.99;
  Matches   75;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;

Qy    608 tgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtgctgcacg 667
          ||||  ||||||   |    |||   |||| ||   ||    |   | ||  | ||||
Db   1434 TGGGGATGGAAGCCGGGAGGAAGCGGCAGGGCAGGGTGACAGTCCCTGCTGCTCAGCACT 1375

Qy    668 atcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctggaaggag 727
            | | |||| | |  |||  | |   |||   |||   | | |   ||   ||||| |
Db   1374 TCCTCAAGACCCAGGGTCGGGGTAGTCCTGCTGGGGAGCTGCCGCCCCAGGGGGAAGTCG 1315

Qy    728 gctgcagtgtgccagtagccgt 749
          |||||   ||| || ||| |
Db   1314 TGTGCAGCCGGCCGGTGGCCAT 1293


RESULT   9
US-09-309-053-8/c
; Sequence 8, Application US/09309053
; Patent No. 6077933
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Mu-En
;    APPLICANT:  McA'Nulty, Megan M.
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;    TITLE OF INVENTION:  REPRESSOR KRUPPEL-LIKE FACTOR
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/309,053
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/946,241
;      FILING DATE:  07-OCT-1997
;      APPLICATION NUMBER:  60/030,035
;      FILING DATE:  05-NOV-1996
;      APPLICATION NUMBER:  60/027,521
;      FILING DATE:  07-OCT-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Creason, Gary L.
;      REGISTRATION NUMBER:  34,310
;      REFERENCE/DOCKET NUMBER:  05433/027001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-542-5070
;      TELEFAX:  617-542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1889 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  407...1843
US-09-309-053-8


  Query Match             3.4%;  Score 34.8;  DB 3;  Length 1889;
  Best Local Similarity   52.8%;  Pred. No. 0.99;
  Matches   75;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;

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Qy     728 gctgcagtgtgccagtagccgt 749
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Db    1314 TGTGCAGCCGGCCGGTGGCCAT 1293


RESULT  10
US-08-073-384C-7
; Sequence 7, Application US/08073384C
; Patent No. 5541311
;  GENERAL INFORMATION:
;    APPLICANT:  Dahlberg, James E.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Brow, Mary Ann D.
;    TITLE OF INVENTION:  SYNTHESIS-DEFICIENT THERMOSTABLE DNA
;    TITLE OF INVENTION:  POLYMERASE
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HAVERSTOCK, MEDLEN & CARROLL
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/073,384C
;      FILING DATE:  04-JUN-1993
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/986,330
;      FILING DATE:  07-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Carroll, Peter G.
;      REGISTRATION NUMBER:  32,837
;      REFERENCE/DOCKET NUMBER:  FORS-00613
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/705-8410
;      TELEFAX:  415/397-8338
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2502 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-073-384C-7


  Query Match             3.3%;  Score 34.4;  DB 1;  Length 2502;
  Best Local Similarity   44.0%;  Pred. No. 1.5;
  Matches  128;  Conservative    0;  Mismatches  163;  Indels    0;  Gaps    0;

Qy     413 agagaaagttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttc 472
           ||||    |||| | | ||   |    |   |    |||   |      |    |||||
Db    1232 AGAGGCTCTTCCNGAACCTNNNGCAGCGCCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTT 1291

Qy     473 ggaagctggacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagc 532
           ||  ||  ||| |||     | | | | | |   ||         ||     |   |
Db    1292 ACCAGGAGGTGGAGAAGCCCCTTTCCCGGGTCCTGGCCCACATGGAGGCCACGGGGGTNC 1351

Qy     533 gcatgggctggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctg 592
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Db    1352 GGCTGGACGTGGCCTACCTCCAGGCCCTNTCCCTGGAGGTGGCGGAGGAGATCCGCCGCC 1411

Qy     593 tgggccaggggggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctgg 652
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Db    1412 TCGAGGAGGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCGGGACCAGC 1471

Qy     653 tgggtgtgctgcacgatcccgagactctgcttcgctgcatcgctgaaaggg 703
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Db    1472 TGGAAAGGGTGCTCTTTGACGAGCTNGGGCTTCCCGCCATCGGCAAGACGG 1522


RESULT  11
US-08-254-359A-7
; Sequence 7, Application US/08254359A
; Patent No. 5614402
;  GENERAL INFORMATION:
;    APPLICANT:  DAHLBERG, JAMES E.
;    APPLICANT:  LYAMICHEV, VICTOR I.
;    APPLICANT:  BROW, MARY ANN D.
;    TITLE OF INVENTION:  5' NUCLEASES DERIVED FROM THERMOSTABLE
;    TITLE OF INVENTION:  DNA POLYMERASE
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HAVERSTOCK, MEDLEN & CARROLL
;      STREET:  220 MONTGOMERY STREET, SUITE 2200
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;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/254,359A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/073,384
;      FILING DATE:  06-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/986,330
;      FILING DATE:  07-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CARROLL, PETER G.
;      REGISTRATION NUMBER:  32,837
;      REFERENCE/DOCKET NUMBER:  FORS-01000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410]
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2502 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-254-359A-7


  Query Match             3.3%;  Score 34.4;  DB 1;  Length 2502;
  Best Local Similarity   44.0%;  Pred. No. 1.5;
  Matches  128;  Conservative    0;  Mismatches  163;  Indels    0;  Gaps    0;

Qy     413 agagaaagttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttc 472
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Db    1232 AGAGGCTCTTCCNGAACCTNNNGCAGCGCCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTT 1291

Qy     473 ggaagctggacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagc 532
             ||  ||  ||| |||     | | | | | |   ||        ||      |   |
Db    1292 ACCAGGAGGTGGAGAAGCCCCTTTCCCGGGTCCTGGCCCACATGGAGGCCACGGGGGTNC 1351

Qy     533 gcatgggctggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctg 592
           |  ||| |  |  | |||     |  |    |||| |    | |||    ||
Db    1352 GGCTGGACGTGGCCTACCTCCAGGCCCTNTCCCTGGAGGTGGCGGAGGAGATCCGCCGCC 1411

Qy     593 tgggccaggggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctgg 652
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Db    1412 TCGAGGAGGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCGGGACCAGC 1471

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Db    1472 TGGAAAGGGTGCTCTTTGACGAGCTNGGGCTTCCCGCCATCGGCAAGACGG 1522


RESULT  12
US-08-483-043-7
; Sequence 7, Application US/08483043
; Patent No. 5691142
;  GENERAL INFORMATION:
;    APPLICANT:  Dahlberg, James E.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Brow, Mary Ann D.
;    TITLE OF INVENTION:  SYNTHESIS-DEFICIENT THERMOSTABLE DNA
;    TITLE OF INVENTION:  POLYMERASE
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HAVERSTOCK, MEDLEN & CARROLL
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/483,043
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/073,384
;      FILING DATE:  04-JUN-1993
;      APPLICATION NUMBER:  US 07/986,330
;      FILING DATE:  07-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Carroll, Peter G.
;      REGISTRATION NUMBER:  32,837
;      REFERENCE/DOCKET NUMBER:  FORS-00613
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/705-8410
;      TELEFAX:  415/397-8338
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2502 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-483-043-7


  Query Match             3.3%;  Score 34.4;  DB 1;  Length 2502;
  Best Local Similarity   44.0%;  Pred. No. 1.5;
  Matches  128;  Conservative    0;  Mismatches  163;  Indels    0;  Gaps    0;

Qy     413 agagaaagttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttc 472
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Qy     473 ggaagctggacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagc 532
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Db    1292 ACCAGGAGGTGGAGAAGCCCCTTTCCCGGGTCCTGGCCCACATGGAGGCCACGGGGGTNC 1351

Qy     533 gcatgggctggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctg 592
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Db    1352 GGCTGGACGTGGCCTACCTCCAGGCCCTNTCCCTGGAGGTGGCGGAGGAGATCCGCCGCC 1411

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Db    1412 TCGAGGAGGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCGGGACCAGC 1471

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RESULT  13
US-08-481-238-7
; Sequence 7, Application US/08481238
; Patent No. 5795763
;  GENERAL INFORMATION:
;    APPLICANT:  DAHLBERG, JAMES E.
;    APPLICANT:  LYAMICHEV, VICTOR I.
;    APPLICANT:  BROW, MARY ANN D.
;    TITLE OF INVENTION:  SYNTHESIS-DEFICIENT THERMOSTABLE DNA
;    TITLE OF INVENTION:  POLYMERASE
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
```

```
;       ADDRESSEE:  MEDLEN & CARROLL
;       STREET:  220 MONTGOMERY STREET, SUITE 2200
;       CITY:  SAN FRANCISCO
;       STATE:  CALIFORNIA
;       COUNTRY:  USA
;       ZIP:  94104
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/481,238
;       FILING DATE:
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  CARROLL, PETER G.
;       REGISTRATION NUMBER:  32,837
;       REFERENCE/DOCKET NUMBER:  FORS-01798
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 705-8410
;       TELEFAX:  (415) 397-8338
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2502 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-481-238-7


  Query Match             3.3%;  Score 34.4;  DB 1;  Length 2502;
  Best Local Similarity   44.0%;  Pred. No. 1.5;
  Matches  128;  Conservative    0;  Mismatches  163;  Indels    0;  Gaps    0;

Qy     413 agagaaagttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttc 472
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Db    1232 AGAGGCTCTTCCNGAACCTNNNGCAGCGCCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTT 1291

Qy     473 ggaagctggacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagc 532
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Db    1292 ACCAGGAGGTGGAGAAGCCCCTTTCCCGGGTCCTGGCCCACATGGAGGCCACGGGGGTNC 1351

Qy     533 gcatgggctggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctg 592
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Db    1352 GGCTGGACGTGGCCTACCTCCAGGCCCTNTCCCTGGAGGTGGCGGAGGAGATCCGCCGCC 1411

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Db    1412 TCGAGGAGGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCGGGACCAGC 1471

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RESULT  14
US-08-471-066B-7
; Sequence 7, Application US/08471066B
; Patent No. 5837450
;  GENERAL INFORMATION:
;    APPLICANT:  Dahlberg, James E.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Brow, Mary Ann D.
;    TITLE OF INVENTION:  5' Nucleases Derived From Thermostable
;    TITLE OF INVENTION:  DNA Polymerase
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;       COUNTRY:  United States of America
;       ZIP:  94104
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/471,066B
;       FILING DATE:  06-JUN-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/254,359
;       FILING DATE:  06-JUN-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/073,384
;       FILING DATE:  04-JUN-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/986,330
;       FILING DATE:  07-DEC-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Ingolia, Diane E.
;       REGISTRATION NUMBER:  40,027
;       REFERENCE/DOCKET NUMBER:  FORS-01800
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 705-8410
;       TELEFAX:  (415) 397-8338
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2502 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-471-066B-7


  Query Match             3.3%;  Score 34.4;  DB 2;  Length 2502;
  Best Local Similarity   44.0%;  Pred. No. 1.5;
  Matches  128;  Conservative    0;  Mismatches  163;  Indels    0;  Gaps    0;

Qy     413 agagaaagttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttc 472
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Db    1232 AGAGGCTCTTCCNGAACCTNNNGCAGCGCCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTT 1291

Qy     473 ggaagctggacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagc 532
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Db    1292 ACCAGGAGGTGGAGAAGCCCCTTTCCCGGGTCCTGGCCCACATGGAGGCCACGGGGGTNC 1351

Qy     533 gcatgggctggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctg 592
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Db    1352 GGCTGGACGTGGCCTACCTCCAGGCCCTNTCCCTGGAGGTGGCGGAGGAGATCCGCCGCC 1411

Qy     593 tgggccaggggcccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctgg 652
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Db    1412 TCGAGGAGGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCGGGACCAGC 1471

Qy     653 tgggtgtgctgcacgatcccgagactctgcttcgctgcatcgctgaaaggg 703
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RESULT  15
US-08-484-956-7
; Sequence 7, Application US/08484956
; Patent No. 5843654
;  GENERAL INFORMATION:
;    APPLICANT:  DAHLBERG, JAMES E.
;    APPLICANT:  LYAMICHEV, VICTOR I.
;    APPLICANT:  BROW, MARY ANN D.
;    APPLICANT:  OLDENBURG, MARY C.
;    APPLICANT:  HEISLER, LAURA
;    TITLE OF INVENTION:  DETECTION OF p53 MUTATIONS
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;    NUMBER OF SEQUENCES:  114
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HAVERSTOCK, MEDLEN & CARROLL
;      STREET:  220 MONTGOMERY STREET, SUITE 2200
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,956
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/402,601
;      FILING DATE:  09-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/337,164
;      FILING DATE:  09-NOV-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/254,359
;      FILING DATE:  06-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/073,384
;      FILING DATE:  04-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/986,330
;      FILING DATE:  07-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CARRPOLL ], PETER G.
;      REGISTRATION NUMBER:  32,837
;      REFERENCE/DOCKET NUMBER:  FORS-01801
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2502 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-484-956-7


  Query Match             3.3%;  Score 34.4;  DB 2;  Length 2502;
  Best Local Similarity   44.0%;  Pred. No. 1.5;
  Matches  128;  Conservative    0;  Mismatches  163;  Indels    0;  Gaps    0;

Qy    413 agagaaagttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttc 472
          ||||    |||| | | ||   |    |   |    |||   |      |    |||||
Db   1232 AGAGGCTCTTCCNGAACCTNNNGCAGCGCCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTT 1291

Qy    473 ggaagctggacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagc 532
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Db   1292 ACCAGGAGGTGGAGAAGCCCCTTTCCCGGGTCCTGGCCCACATGGAGGCCACGGGGGTNC 1351

Qy    533 gcatgggctggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctg 592
          |  ||| |  |  | |||     | |    |||| |    | |||   ||
Db   1352 GGCTGGACGTGGCCTACCTCCAGGCCCTNTCCCTGGAGGTGGCGGAGGAGATCCGCCGCC 1411

Qy    593 tgggccaggggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctgg 652
          | |   ||| || |||  || |||  | |   ||    |||   ||  |  ||| | |
Db   1412 TCGAGGAGGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCGGGACCAGC 1471

Qy    653 tgggtgtgctgcacgatcccgagactctgcttcgctgcatcgctgaaaggg 703
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Db   1472 TGGAAAGGGTGCTCTTTGACGAGCTNGGGCTTCCCGCCATCGGCAAGACGG 1522
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Job time: 120 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: October 6, 2001, 19:04:54 ; Search time 1970.35 Seconds
(without alignments)
5339.674 Million cell updates/sec

Title: US-09-601-138-12
Perfect score: 1113
Sequence: 1 cacacagcctactttccaag.....aattgaacgatgcccattaa 1113

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
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257: gb_gss36:*
258: gb_gss37:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	870.8	78.2	1036	105	AL520285	AL520285 AL520285
2	837.4	75.2	882	105	AL524270	AL524270 AL524270
3	756.4	68.0	942	106	AL557370	AL557370 AL557370
4	728.4	65.4	904	152	BG337601	BG337601 602435148
5	724.4	65.1	835	154	BG469642	BG469642 602533692
c 6	711.4	63.9	949	106	AL561865	AL561865 AL561865
7	706.2	63.5	1136	137	BE561357	BE561357 601344923
8	698.2	62.7	878	105	AL516000	AL516000 AL516000
9	688.2	61.8	812	108	AU132868	AU132868 AU132868
c 10	682	61.3	838	106	AL579416	AL579416 AL579416
11	671.4	60.3	804	137	BE547860	BE547860 601074758
c 12	659.2	59.2	919	105	AL520284	AL520284 AL520284
13	657.8	59.1	1087	137	BE561038	BE561038 601344655
14	654.6	58.8	908	105	AL520223	AL520223 AL520223
15	651	58.5	970	172	BF971877	BF971877 602240467
16	650.4	58.4	801	143	BF035760	BF035760 601458755
c 17	628.8	56.5	941	106	AL561775	AL561775 AL561775
18	627.4	56.4	693	140	BE795040	BE795040 601592839
19	626	56.2	869	141	BE870723	BE870723 601448575
20	617.8	55.5	795	141	BE905261	BE905261 601499109
c 21	602.2	54.1	746	106	AL562330	AL562330 AL562330
22	593.2	53.3	807	108	AU143511	AU143511 AU143511
23	587.2	52.8	883	107	AU118927	AU118927 AU118927
24	586	52.7	695	136	BE514746	BE514746 601317044
25	584	52.5	666	167	BE396412	BE396412 601288795
26	569.4	51.2	873	152	BG336990	BG336990 602434444
27	568.8	51.1	1090	175	BG257063	BG257063 602370616
28	561.8	50.5	1087	152	BG338518	BG338518 602436243
29	560.6	50.4	840	18	AI325891	AI325891 mg10e04.y
30	557.4	50.1	849	152	BG339222	BG339222 602437086
c 31	557	50.0	755	105	AL515999	AL515999 AL515999
32	543	48.8	847	153	BG421936	BG421936 602449682
33	531.4	47.7	968	141	BE889503	BE889503 601512410
34	530	47.6	893	137	BE561477	BE561477 601346541
35	522.8	47.0	538	172	BG025746	BG025746 602274731
36	521.8	46.9	776	106	AL531360	AL531360 AL531360
37	518.4	46.6	622	141	BE870227	BE870227 601449952
38	517.6	46.5	784	140	BE790191	BE790191 601480431
39	511	45.9	593	153	BG385710	BG385710 602454134
40	509	45.7	963	174	BG180160	BG180160 602329751
41	504.8	45.4	807	107	AU120403	AU120403 AU120403
42	503.8	45.3	882	145	BF183906	BF183906 601842703
43	495.6	44.5	797	15	AI048619	AI048619 ud64a04.y
44	494.4	44.4	891	140	BE785743	BE785743 601478516
45	494	44.4	658	145	BF204322	BF204322 601867791

ALIGNMENTS

RESULT 1
AL520285
LOCUS AL520285 1036 bp mRNA EST 13-FEB-2001
DEFINITION AL520285 LTI_NFL004_NBC2 Homo sapiens cDNA clone CS0DB006YG07 5 prime, mRNA sequence.
ACCESSION AL520285
VERSION AL520285.1 GI:12783778
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1036)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES Location/Qualifiers
source 1. .1036
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DB006YG07"
/clone_lib="LTI_NFL004_NBC2"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
BASE COUNT 243 a 282 c 310 g 200 t 1 others
ORIGIN

Query Match 78.2%; Score 870.8; DB 105; Length 1036;
Best Local Similarity 99.0%; Pred. No. 5.1e-223;
Matches 927; Conservative 1; Mismatches 3; Indels 5; Gaps 5;

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Qy      1 cacacagcctactttccaagcggagccatgtctggtaacggcaatgcggctgcaacggcg 60
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Db    102 CACACAGCCTACTTTCCAAGCGGA-CCATGTCTGGTAACGGCAATGCGGCTGCAACGGCG 160

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Db    161 GAAGAAAACAGCCCAAAGATGAGAGTGATTCGCGTGGGTACCCGCAAGAGCCAGCTTGCT 220

Qy    121 cgcatacagacggacagtgtggtggcaacattgaaagcctcgtaccctggcctgcagttt 180
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Db    221 CGCATACAGACGGACAGTGTGGTGGCAACATTGAAAGCCTCGTACCCTGGCCTGCAGTTT 280

Qy    181 gaaatcattgctatgtccaccacaggggacaagattcttgatactgcactctctaagatt 240
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Qy    241 ggagagaaaagcctgtttaccaaggagcttgaacatgccctggagaagaatgaagtggac 300
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Db    341 GGAGAGAAAAGCCTGTTTACCAAGGAGCTTGAACATGCCCTGGAGAAGAATGAAGTGGAC 400

Qy    301 ctggttgttcactccttgaaggacctgcccactgtgcttcctcctggcttcaccatcgga 360
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Qy    361 gccatctgcaagcgggaaaaccctcatgatgctgttgtctttcacccaaaatttgttggg 420
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Qy    421 aagaccctagaaaccctgccagagaagagtgtggtgggaaccagctccctgcgaagagca 480
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Db    521 AAGACCCTAGAAACCCTGCCAGAGAAGAGTGTGGTGGGAACCAGCTCCCTGCGAAGAGCA 580

Qy    481 gcccagctgcagagaaagttcccgcatctggagttcaggagtattcggggaaacctcaac 540
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Db    581 GCCCAGCTGCAGAGAAAGTTCCCGCATCTGGAGTTCAGGAGTATTCGGGGAAACCTCAAC 640

Qy    541 acccggcttcggaagctggacgagcagcaggagttcagtgccatcatcctggcaacagct 600
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Db    641 ACCCGGCTTCGGAAGCTGGACGAGCAGCAGGAGTTCAGTGCCATCATCCTGGCAACAGCT 700

Qy    601 ggcctgcagcgcatgggctggcacaaccgggttgggcagatcctgcaccctgaggaatgc 660
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Qy    781 gccttcctgaggcacctggaaggaggctgcagtgtgccagtagccgtgcatacagctatg 840
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Qy    841 aaggatgggcaactgtacctgactggaggagtctggagtctagacggctcagatagcata 900
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Qy    901 caagagaccatgcaggctaccatccatgtccctgcc 936
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Db    999 CAAGAGA-CATGCAGGCTA-CATCCATGTCCCGCCC 1032
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RESULT 2
AL524270
LOCUS AL524270 882 bp mRNA EST 13-FEB-2001
DEFINITION AL524270 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC002YJ01 5 prime, mRNA sequence.
ACCESSION AL524270
VERSION AL524270.1 GI:12787763
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 882)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES Location/Qualifiers
source 1. .882
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DC002YJ01"
/clone_lib="LTI_NFL003_NBC3"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
BASE COUNT 205 a 236 c 262 g 178 t 1 others
ORIGIN

Query Match 75.2%; Score 837.4; DB 105; Length 882;
Best Local Similarity 99.2%; Pred. No. 4.5e-214;
Matches 852; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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Qy    313 tccttgaaggacctgcccactgtgcttcctcctggcttcaccatcggagccatctgcaag 372
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Qy    373 cgggaaaaccctcatgatgctgttgtctttcacccaaaatttgttgggaagaccctagaa 432
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Db    121 CGGGAAAACCCTCATGATGCTGTTGTCTTTCACCCAAAATTTGTTGGGAAGACCCTAGAA 180

Qy    433 accctgccagagaagagtgtggtgggaaccagctccctgcgaagagcagcccagctgcag 492
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Db    181 ACCCTGCCAGAGAAGAGTGTGGTGGGAACCAGCTCCCTGCGAAGAGCAGCCCAGCTGCAG 240

Qy    493 agaaagttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttcgg 552
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Qy    553 aagctggacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgc 612
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Qy    613 atgggctggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctgtg 672
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Qy    793 cacctggaaggaggctgcagtgtgccagtagccgtgcatacagctatgaaggatgggcaa 852
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Db    541 CACCTGGAA-GAGGCTGCAGTGTGCCAGTAGCCGTGCATACAGCTATGAAGGATGGGCAA 599

Qy    853 ctgtacctgactggaggagtctggagtctagacggctcagatagcatacaagagaccatg 912
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    600 CTGTACCTGACTGGAGGAGTCTGGAGTCTAGACGGCTCAGATAGCATACAAGAGACCATG 659

Qy    913 caggctaccatccatgtccctgcccagcatgaagatggccctgaggatgacccacagttg 972
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    660 CAGGCTACCATCCATGTCCCTGCCCAGCATGAAGATGGCCCTGAGGATGACCCACAGTTG 719

Qy    973 gtaggcatcactgctcgtaacattccacgagggccccagttggctgcccagaacttgggc 1032
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    720 GTAGGCATCACTGCTCGTAACAATCCACGAGGGCCCCAGTTGGCTGCCCAGAACTTGGGC 779

Qy   1033 atcagcctggccaacttgttgctgagcaaaggagccaaaaacatcctggatgttgcacgg 1092
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    780 ATCAGCCTGGCCAACTTGTTGCTGAGCAAAGGAGCCAAAAACATCCTGGATGTTGCACGG 839

Qy   1093 caattgaacgatgcccatt 1111
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Db    840 CAGCCTAACGATGCCCATT 858
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RESULT 3
AL557370
LOCUS AL557370 942 bp mRNA EST 16-FEB-2001
DEFINITION AL557370 LTI_FL012_TC1 Homo sapiens cDNA clone CS0DH004YP13 5 prime, mRNA sequence.
ACCESSION AL557370
VERSION AL557370.1 GI:12900909
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 942)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)

```
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .942
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DH004YP13"
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                     /tissue_type="T cells from T cell leukemia"
                     /lab_host="DH10B"
                     /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-stranded cDNA was digested with Not I and cloned
                     into the Not I and Eco RV sites of the pCMVSPORT 6 vector.
                     Library was constructed by Life Technologies. Contact :
                     Feng Liang Life Technologies, a division of Invitrogen
                     9800 Medical Center Drive Rockville, Maryland 20850, USA
                     Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      216 a    258 c    284 g    183 t      1 others
ORIGIN


  Query Match             68.0%;  Score 756.4;  DB 106;  Length 942;
  Best Local Similarity   98.4%;  Pred. No. 2.6e-192;
  Matches  805;  Conservative    1;  Mismatches    7;  Indels    5;  Gaps    4;

Qy       1 cacacagcctactttccaagcggagccatgtctggtaacggcaatgcggctgcaacggcg 60
           |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db     114 CACACAGCCTACTTTCCAAGCGGA-CCATGTCTGGTAACGGCAATGCGGCTGCAACGGCG 172

Qy      61 gaagaaaacagcccaaagatgagagtgattcgcgtgggtacccgcaagagccagcttgct 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     173 GAAGAAAACAGCCCAAAGATGAGAGTGATTCGCGTGGGTACCCGCAAGAGCCAGCTTGCT 232

Qy     121 cgcatacagacggacagtgtggtggcaacattgaaagcctcgtaccctggcctgcagttt 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     233 CGCATACAGACGGACAGTGTGGTGGCAACATTGAAAGCCTCGTACCCTGGCCTGCAGTTT 292

Qy     181 gaaatcattgctatgtccaccacaggggacaagattcttgatactgcactctctaagatt 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     293 GAAATCATTGCTATGTCCACCACAGGGGACAAGATTCTTGATACTGCACTCTCTAAGATT 352

Qy     241 ggagagaaaagcctgtttaccaaggagcttgaacatgccctggagaagaatgaagtggac 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     353 GGAGAGAAAAGCCTGTTTACCAAGGAGCTTGAACATGCCCTGGAGAAGAATGAAGTGGAC 412

Qy     301 ctggttgttcactccttgaaggacctgcccactgtgcttcctcctggcttcaccatcgga 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     413 CTGGTTGTTCACTCCTTGAAGGACCTGCCCACTGTGCTTCCTCCTGGCTTCACCATCGGA 472

Qy     361 gccatctgcaagcgggaaaaccctcatgatgctgttgtctttcacccaaaatttgttggg 420
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Db     473 GCCATCTGCAAGCGGGAAAACCCTCATGATGCTGTTGTCTTTCACCCAAAATTTGTTGGG 532

Qy     421 aagaccctagaaaccctgccagagaagagtgtggtgggaaccagctccctgcgaagagca 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     533 AAGACCCTAGAAACCCTGCCAGAGAAGAGTGTGGTGGGAACCAGCTCCCTGCGAAGAGCA 592

Qy     481 gcccagctgcagagaaagttcccgcatctggagttcaggagtattcggggaaacctcaac 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     593 GCCCAGCTGCAGAGAAAGTTCCCGCATCTGGAGTTCAGGAGTATTCGGGGAAACCTCAAC 652

Qy     541 acccggcttcggaagctggacgagcagcaggagttcagtgccatcatcctggcaacagct 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     653 ACCCGGCTTCGGAAGCTGGACGAGCAGCAGGAGTTCAGTGCCATCATCCTGGCAACAGCT 712

Qy     601 ggcctgcagcgcatg-ggctggcacaaccgggttgggcagatcctgcaccctgaggaatg 659
           ||||||||||||||| |||||||||||||||| ||||||||||||||||||||||||||
Db     713 GGCCTGCAGCGCATGTGGCTGGCACAACCGGGTGGGGCAGATCCTGCACCCTGAGGAATG 772

Qy     660 catgtatgctgtgggccaggggccttgggcgtggaagtgcgagccaaggaccaggacat 719
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     773 CATGTATGCTGTGGGCCAGGGGG-CTTGGGCGTGGAAGTGCGAGCCAAGGACCAGGACAT 831

Qy     720 cttggatctggtgggtgtgctgcacgatcccgagactctgcttcgctgcatcgctgaaag 779
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     832 CTTGGATCTGGTGGGTGTGCTGCACGATCCCGAGACTCTGCTTCGCTGCATCGCTGAAAG 891

Qy     780 ggccttcctgaggcacctggaaggaggctgcagtgtgc 817
           |||:||||||||    |  | | ||||||||||||||
Db     892 GGCYTTCCTGAG--CACCTGGAAGAGGCTGCAGTGTGC 927


RESULT   4
BG337601
LOCUS       BG337601      904 bp    mRNA            EST       27-FEB-2001
DEFINITION  602435148F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4553315 5',
            mRNA sequence.
ACCESSION   BG337601
VERSION     BG337601.1  GI:13144039
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 904)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1250  row: o  column: 12
            High quality sequence stop: 768.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC_46"
                     /tissue_type="leiomyosarcoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using  ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."
BASE COUNT      212 a    234 c    285 g    171 t      2 others
ORIGIN


  Query Match             65.4%;  Score 728.4;  DB 152;  Length 904;
  Best Local Similarity   98.6%;  Pred. No. 8.4e-185;
  Matches  765;  Conservative    0;  Mismatches    8;  Indels    3;  Gaps    3;

Qy     233 ctaagattggagagaaaagcctgtttaccaaggagcttgaacatgccctggagaagaatg 292
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 CTAAGATTGGAGAGAAAAGCCTGTTTACCAAGGAGCTTGAACATGCCCTGGAGAAGAATG 61

Qy     293 aagtggacctggttgttcactccttgaaggacctgcccactgtgcttcctcctggcttca 352
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 AAGTGGACCTGGTTGTTCACTCCTTGAAGGACCTGCCCACTGTGCTTCCTCCTGGCTTCA 121
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Qy    353 ccatcggagccatctgcaagcgggaaaaccctcatgatgctgttgtctttcacccaaaat 412
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122 CCATCGGAGCCATCTGCAAGCGGGAAAACCCTCATGATGCTGTTGTCTTTCACCCAAAAT 181

Qy    413 ttgttgggaagaccctagaaaccctgccagagaagagtgtggtgggaaccagctccctgc 472
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    182 TTGTTGGGAAGACCCTAGAAACCCTGCCAGAGAAGAGTGTGGTGGGAACCAGCTCCCTGC 241

Qy    473 gaagagcagcccagctgcagagaaagttcccgcatctggagttcaggagtattcggggaa 532
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    242 GAAGAGCAGCCCAGCTGCAGAGAAAGTTCCCGCATCTGGAGTTCAGGAGTATTCGGGGAA 301

Qy    533 acctcaacacccggcttcggaagctggacgagcagcaggagttcagtgccatcatcctgg 592
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Db    302 ACCTCAACACCCGGCTTCGGAAGCTGGACGAGCAGCAGGAGTTCAGTGCCATCATCCTGG 361

Qy    593 caacagctggcctgcagcgcatgggctggcacaaccgggttgggcagatcctgcaccctg 652
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Db    362 CAACAGCTGGCCTGCAGCGCATGGGCTGGCACAACCGGGTGGGGCAGATCCTGCACCCTG 421

Qy    653 aggaatgcatgtatgctgtgggccaggggccttgggcgtggaagtgcgagccaaggacc 712
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Db    422 AGGAATGCATGTATGCTGTGGGCCAGGGGGCCTTGGGCGTGGAAGTGCGAGCCAAGGACC 481

Qy    713 aggacatcttggatctggtgggtgtgctgcacgatcccgagactctgcttcgctgcatcg 772
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Db    482 AGGACATCTTGGATCTGGTGGGTGTGCTGCACGATCCCGAGACTCTGCTTCGCTGCATCG 541

Qy    773 ctgaaagggccttcctgaggcacctggaaggaggctgcagtgtgccagtagccgtgcata 832
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    542 CTGAAAGGGCCTTCCTGAGGCACCTGGAAGGAGGCTGCAGTGTGCCAGTAGCCGTGCATA 601

Qy    833 cagctatgaaggatgggcaactgtacctgactggaggagtctggagtctagacggctcag 892
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| | ||||
Db    602 CAGCTATGAAGGATGGGCAACTGTACCTGACTGGAGGAGTCTGGAGTCTAGACNGGTCAG 661

Qy    893 atagcatacaagagaccatgcaggctaccatccatgtccctgcccagcatgaagatggcc 952
          |||||||||||||||||||||||||||| ||||||||| |||| |||||||||||||| |
Db    662 ATAGCATACAAGAGACCATGCAGGCTA-CATCCATGTTCCTGTCCAGCATGAAGATGGNC 720

Qy    953 ctgaggatgacccacagttggtaggcatcactgctcgtaacattccacgagggccc 1008
          |||||||||| |||||||||||||||| |||||| |||||||||||||||||| |||
Db    721 CTGAGGATGA-CCACAGTTGGTAGGC-TCACTGGTCGTAACATTCCACGAGGCCCC 774


RESULT  5
BG469642
LOCUS       BG469642      835 bp    mRNA            EST       21-MAR-2001
DEFINITION  602533692F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4661422 5',
            mRNA sequence.
ACCESSION   BG469642
VERSION     BG469642.1  GI:13401917
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 835)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: NIH Intramural Sequencing Center
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1460  row: g  column: 23
            High quality sequence stop: 824.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4661422"
                     /clone_lib="NIH_MGC_15"
                     /tissue_type="adenocarcinoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)"
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ORIGIN


  Query Match           65.1%;  Score 724.4;  DB 154;  Length 835;
  Best Local Similarity  99.6%;  Pred. No. 9.8e-184;
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Db     85 CACACAGCCTACTTTCCAAGCGGAGCCATGTCTGGTAACGGCAATGCGGCTGCAACGGCG 144

Qy     61 gaagaaaacagcccaaagatgagagtgattcgcgtgggtacccgcaagagccagcttgct 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    145 GAAGAAAACAGCCCAAAGATGAGAGTGATTCGCGTGGGTACCCGCAAGAGCCAGCTTGCT 204

Qy    121 cgcatacagacggacagtgtggtggcaacattgaaagcctcgtaccctggcctgcagttt 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    205 CGCATACAGACGGACAGTGTGGTGGCAACATTGAAAGCCTCGTACCCTGGCCTGCAGTTT 264

Qy    181 gaaatcattgctatgtccaccacaggggacaagattcttgatactgcactctctaagatt 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    265 GAAATCATTGCTATGTCCACCACAGGGGACAAGATTCTTGATACTGCACTCTCTAAGATT 324

Qy    241 ggagagaaaagcctgtttaccaaggagcttgaacatgccctggagaagaatgaagtggac 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    325 GGAGAGAAAAGCCTGTTTACCAAGGAGCTTGAACATGCCCTGGAGAAGAATGAAGTGGAC 384

Qy    301 ctggttgttcactccttgaaggacctgcccactgtgcttcctcctggcttcaccatcgga 360
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Qy    361 gccatctgcaagcgggaaaaccctcatgatgctgttgtctttcacccaaaatttgttggg 420
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Qy    421 aagaccctagaaaccctgccagagaagagtgtggtgggaaccagctccctgcgaagagca 480
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Db    505 AAGACCCTAGAAACCCTGCCAGAGAAGAGTGTGGTGGGAACCAGCTCCCTGCGAAGAGCA 564

Qy    481 gcccagctgcagagaaagttcccgcatctggagttcaggagtattcggggaaacctcaac 540
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Db    565 GCCCAGCTGCAGAGAAAGTTCCCGCATCTGGAGTTCAGGAGTATTCGGGGAAACCTCAAC 624

Qy    541 acccggcttcggaagctggacgagcagcaggagttcagtgccatcatcctggcaacagct 600
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Db    625 ACCCGGCTTCGGAAGCTGGACGAGCAGCAGGAGTTCAGTGCCATCATCCTGGCAACAGCT 684

Qy    601 ggcctgcagcgcatgggctggcacaaccgggttgggcagatcctgcaccctgaggaatgc 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    685 GGCCTGCAGCGCATGGGCTGGCACAACCGGGTTGGGCAGATCCTGCACCCTGAGGAATGC 744

Qy    661 atgtatgctgtgggccaggggccttgggcg-tggaagtgcgagccaaggaccaggacat 719
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    745 ATGTATGCTGTGGGCCAGGGGGCCTTGGGCGTTGGAAGTGCGAGCCAAGGACCAGGACAT 804

Qy    720 cttggatctggtgggtgtgctgcacgatcc 749
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Db    805 CTTGGATCT-GTGGGTGTGCTGAACGATCC 833


RESULT   6
AL561865/c
LOCUS       AL561865      949 bp    mRNA            EST       16-FEB-2001
DEFINITION  AL561865 LTI_NFL004_NBC2 Homo sapiens cDNA clone CS0DB006YI03 3
            prime, mRNA sequence.
ACCESSION   AL561865
VERSION     AL561865.1  GI:12909719
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 949)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .949
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                     /db_xref="taxon:9606"
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                     /clone_lib="LTI_NFL004_NBC2"
                     /sex="male"
                     /tissue_type="neuroblastoma cells"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector.  Library was normalized. Library was constructed
                     by Life Technologies.  Contact : Feng Liang Life
                     Technologies, a division of Invitrogen 9800 Medical Center
                     Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
                     8371 Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      196 a    277 c    265 g    207 t      4 others
ORIGIN


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  Best Local Similarity   98.6%;  Pred. No. 3.1e-180;
  Matches  756;  Conservative    3;  Mismatches    4;  Indels    4;  Gaps    4;

Qy    347 gcttcaccatcggagccatctgcaagcgggaaaaccctcatgatgctgttgtctttcacc 406
          ||||||||||||||||||||:|||| |||||||||||||||||||||| ||||||
Db    940 GCTTCACCATCGGAGCCATCTGMAAGC-GGAAAACCCTCATGATGCTGTTGTC-TTCACC 883

Qy    407 caaaatttgttgggaagaccctagaaaccctgccagagaagagtgtggtgggaaccagct 466
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    882 CAAAATTTGTT-GGAAGACCCTAGAAACCCTGCCAGAGAAGAGTGTGGTGGGAACCAGCT 824

Qy    467 ccctgcgaagagcagcccagctgcagagaaagttcccgcatctggagttcaggagtattc 526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    823 CCCTGCGAAGAGCAGCCCAGCTGCAGAGAAAGTTCCCGCATCTGGAGTTCAGGAGTATTC 764

Qy    527 ggggaaacctcaacacccggcttcggaagctggacgagcagcaggagttcagtgccatca 586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    763 GGGGAAACCTCAACACCCGGCTTCGGAAGCTGGACGAGCAGCAGGAGTTCAGTGCCATCA 704

Qy    587 tcctggcaacagctggcctgcagcgcatgggctggcacaaccgggttgggcagatcctgc 646
          |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db    703 TCCTGGCAACAGCTGGCCTGCAGCGCATGGGCTGGCACAACCGGGTGGGGCAGATCCTGC 644

Qy    647 accctgaggaatgcatgtatgctgtgggccaggggccttgggcgtggaagtgcgagcca 706
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    643 ACCCTGAGGAATGCATGTATGCTGTGGGCCAGGGGGCCTTGGGCGTGGAAGTGCGAGCCA 584

Qy    707 aggaccaggacatcttggatctggtgggtgtgctgcacgatcccgagactctgcttcgct 766
          |||||||:||||||||:||||||||||||||||||||||||||||||||| |||||||
Db    583 AGGACCARGACATCTTRGATCTGGTGGGTGTGCTGCACGATCCCGAGACTCT-CTTCGCT 525

Qy    767 gcatcgctgaaagggccttcctgaggcacctggaaggaggctgcagtgtgccagtagccg 826
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    524 GCATCGCTGAAAGGGCCTTCCTGAGGCACCTGGAAGGAGGCTGCAGTGTGCCAGTAGCCG 465

Qy    827 tgcatacagctatgaaggatgggcaactgtacctgactggaggagtctggagtctagacg 886
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    464 TGCATACAGCTATGAAGGATGGGCAACTGTACCTGACTGGAGGAGTCTGGAGTCTAGACG 405

Qy    887 gctcagatagcatacaagagaccatgcaggctaccatccatgtccctgcccagcatgaag 946
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    404 GCTCAGATAGCATACAAGAGACCATGCAGGCTACCATCCATGTCCCTGCCCAGCATGAAG 345

Qy    947 atggccctgaggatgacccacagttggtaggcatcactgctcgtaacattccacgagggc 1006
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    344 ATGGCCCTGAGGATGACCCACAGTTGGTAGGCATCACTGCTCGTAACATTCCACGAGGGC 285

Qy   1007 cccagttggctgcccagaacttgggcatcagcctggccaacttgttgctgagcaaaggag 1066
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    284 CCCAGTTGGCTGCCCAGAACTTGGGCATCAGCCTGGCCAACTTGTTGCTGAGCAAAGGAG 225

Qy   1067 ccaaaaacatcctggatgttgcacggcaattgaacgatgcccattaa 1113
          |||||||||||||||||||||||||||||  | ||||||||||||||
Db    224 CCAAAAACATCCTGGATGTTGCACGGCAGCTTAACGATGCCCATTAA 178


RESULT   7
BE561357
LOCUS       BE561357      1136 bp    mRNA            EST       15-AUG-2000
DEFINITION  601344923F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677764 5',
            mRNA sequence.
ACCESSION   BE561357
VERSION     BE561357.1  GI:9805077
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1136)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM353  row: n  column: 05
            High quality sequence stop: 714.
FEATURES             Location/Qualifiers
     source          1. .1136
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:3677764"
                     /clone_lib="NIH_MGC_8"
                     /tissue_type="Burkitt lymphoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      280 a    298 c    341 g    217 t
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ORIGIN

  Query Match           63.5%;  Score 706.2;  DB 137;  Length 1136;
  Best Local Similarity  95.2%;  Pred. No. 8.1e-179;
  Matches  770;  Conservative    0;  Mismatches   13;  Indels   26;  Gaps    3;

Qy      22 ggagccatgtctggtaacggcaatgcggctgcaacggcggaagaaaacagcccaaagatg 81
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GGAGCCATGTCTGGTAACGGCAATGCGGCTGCAACGGCGGAAGAAAACAGCCCAAAGATG 60

Qy      82 agagtgattcgcgtgggtacccgcaagagccagcttgctcgcatacagacggacagtgtg 141
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AGAGTGATTCGCGTGGGTACCCGCAAGAGCCAGCTTGCTCGCATACAGACGGACAGTGTG 120

Qy     142 gtggcaacattgaaagcctcgtaccctggcctgcagtttgaaatcattgctatgtccacc 201
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GTGGCAACATTGAAAGCCTCGTACCCTGGCCTGCAGTTTGAAATCATTGCTATGTCCACC 180

Qy     202 acaggggacaagattcttgatactgcactctctaagattggagagaaaagcctgtttacc 261
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ACAGGGGACAAGATTCTTGATACTGCACTCTCTAAGATTGGAGAGAAAAGCCTGTTTACC 240

Qy     262 aaggagcttgaacatgccctggagaagaatgaagtggacctggttgttcactccttgaag 321
           ||||||||||||||||||||||||||||||||||||                      |
Db     241 AAGGAGCTTGAACATGCCCTGGAGAAGAATGAAGT----------------------G 276

Qy     322 gacctgcccactgtgcttcctcctggcttcaccatcggagccatctgcaagcgggaaaac 381
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     277 GACCTGCCCACTGTGCTTCCTCCTGGCTTCACCATCGGAGCCATCTGCAAGCGGGAAAAC 336

Qy     382 cctcatgatgctgttgtctttcacccaaaatttgttgggaagaccctagaaaccctgcca 441
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     337 CCTCATGATGCTGTTGTCTTTCACCCAAAATTTGTTGGGAAGACCCTAGAAACCCTGCCA 396

Qy     442 gagaagagtgtggtgggaaccagctccctgcgaagagcagcccagctgcagagaaagttc 501
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     397 GAGAAGAGTGTGGTGGGAACCAGCTCCCTGCGAAGAGCAGCCCAGCTGCAGAGAAAGTTC 456

Qy     502 ccgcatctggagttcaggagtattcggggaaacctcaacacccggcttcggaagctggac 561
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     457 CCGCATCTGGAGTTCAGGAGTATTCGGGGAAACCTCAACACCCGGCTTCGGAAGCTGGAC 516

Qy     562 gagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatgggctgg 621
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     517 GAGCAGCAGGAGTTCAGTGCCATCATCCTGGCAACAGCTGGCCTGCAGCGCATGGGCTGG 576

Qy     622 cacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgc-tgtgggccaggg 680
           |||||||||| |||||||||||||||||||||||||||||||||| ||||||||||||
Db     577 CACAACCGGGTGGGGCAGATCCTGCACCCTGAGGAATGCATGTATGCTTGTGGGCCAGGG 636

Qy     681 ggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtgct 740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     637 GGCCTTGGGCGTGGAAGTGCGAGCCAAGGACCAGGACATCTTGGATCTGGTGGGTGTGCT 696

Qy     741 gcacgatcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctgga 800
           |||||||||||||||||||||||| || |||||||||||||| | |   ||||||  |||
Db     697 GCACGATCCCGAGACTCTGCTTCGGTGGATCGCTGAAAGGGCTTCCTGAAGGCACTGGGA 756

Qy     801 agga-ggctgcagtgtgccagtagccgtg 828
           |||| || ||||||||||||||| ||| |
Db     757 AGGAGGGTTGCAGTGTGCCAGTACCCGGG 785


RESULT   8
AL516000
LOCUS       AL516000      878 bp    mRNA            EST       13-FEB-2001
DEFINITION  AL516000 LTI_NFL011_NBC1 Homo sapiens cDNA clone CS0DA005YC03 5
            prime, mRNA sequence.
ACCESSION   AL516000
VERSION     AL516000.1  GI:12779493
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 878)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .878
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                     /db_xref="taxon:9606"
                     /clone="CS0DA005YC03"
                     /clone_lib="LTI_NFL011_NBC1"
                     /sex="male"
                     /tissue_type="neuroblastoma cells"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector.  Library is not normalized, but is the control for
                     the normalized libraries. Library was constructed by Life
                     Technologies.  Contact : Feng Liang Life Technologies, a
                     division of Invitrogen 9800 Medical Center Drive Rockville
                     , Maryland 20850, USA Fax : (1) 301 610 8371 Email :
                     fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      200 a    235 c    264 g    173 t      6 others
ORIGIN


  Query Match           62.7%;  Score 698.2;  DB 105;  Length 878;
  Best Local Similarity  94.3%;  Pred. No. 1.1e-176;
  Matches  746;  Conservative    4;  Mismatches    2;  Indels   39;  Gaps    1;

Qy     114 gcttgctcgcatacagacggacagtgtggtggcaacattgaaagcctcgtaccctggcct 173
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     127 GCTTGCTCGCATACAGACGGACAGTGTGGTGGCAACATTGAAAGCCTCGTACCCTGGCCT 186

Qy     174 gcagtttgaaatcattgctatgtccaccacaggggacaagattcttgatactgcactctc 233
           ||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db     187 GCAGTTTGAAATCATTGCTATGTCCACCACAGGGGACAAGATTYTTGATACTGCACTCTC 246

Qy     234 taagattggagagaaaagcctgtttaccaaggagcttgaacatgccctggagaagaatga 293
           |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     247 TAARATTGGAGAGAAAAGCCTGTTTACCAAGGAGCTTGAACATGCCCTGGAGAAGAATGA 306

Qy     294 agtggacctggttgttcactccttgaaggacctgcccactgtgcttcctcctggcttcac 353
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     307 AGTGGACCTGGTTGTTCACTCCTTGAAGGACCTGCCCACTGTGCTTCCTCCTGGCTTCAC 366

Qy     354 catcggagccatctgcaagcgggaaaaccctcatgatgctgttgtctttcacccaaaatt 413
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     367 CATCGGAGCCATCTGCAAGCGGGAAAACCCTCATGATGCTGTTGTCTTTCACCCAAAATT 426

Qy     414 tgttgggaagaccctagaaaccctgccagagaagagtgtggtgggaaccagctccctgcg 473
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     427 TGTTGGGAAGACCCTAGAAACCCTGCCAGAGAAGAGTGTGGTGGGAACCAGCTCCCTGCG 486

Qy     474 aagagcagcccagctgcagagaaagttcccgcatctggagttcaggagtattcggggaaa 533
           |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db     487 AAGAGCAGCCCAGCTGCAGAGAAAGTTCCCGCATCTGGAGTACAGGAGTATTCGGGGAAA 546

Qy     534 cctcaacacccggcttcggaagctggacgagcagcaggagttcagtgccatcatcctggc 593
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     547 CCTCAACACCCGGCTTCGGAAGCTGGACGAGCAGCAGGAGTTCAGTGCCATCATCCTGGC 606

Qy     594 aacagctggcctgcagcgcatgggctggcacaaccgggttgggcagatcctgcaccctga 653
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Db    607 AACAGCTGGCCTGCAGCGCATGGGCTGGCACAACCGG---------------------- 643

Qy    654 ggaatgcatgtatgctgtgggccaggggggccttgggcgtggaagtgcgagccaaggacca 713
                      ||||| ||||||||||||||||||||||||||||||||||||||||
Db    644 ---------------GTGGGGCAGGGGGCCTTGGGCGTGGAAGTGCGAGCCAAGGACCA 687

Qy    714 ggacatcttggatctggtgggtgtgctgcacgatcccgagactctgcttcgctgcatcgc 773
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    688 GGACATCTTGGATCTGGTGGGTGTGCTGCACGATCCCGAGACTCTGCTTCGCTGCATCGC 747

Qy    774 tgaaagggccttcctgaggcacctggaaggaggctgcagtgtgccagtagccgtgcatac 833
          ||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db    748 TGAAAGGGCCTTCCTGAGGCACCTGGAAGGAGGCTGCAGTGTGCCAGTWGCCGTGCATAC 807

Qy    834 agctatgaaggatgggcaactgtacctgactggaggagtctggagtctagacggctcaga 893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    808 AGCTATGAAGGATGGGCAACTGTACCTGACTGGAGGAGTCTGGAGTCTAGACGGCTCAGA 867

Qy    894 tagcatacaag 904
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Db    868 TAGCATAMAAG 878
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RESULT  9
AU132868
LOCUS       AU132868      812 bp    mRNA            EST       24-OCT-2000
DEFINITION  AU132868 NT2RP4 Homo sapiens cDNA clone NT2RP4000750 5', mRNA
            sequence.
ACCESSION   AU132868
VERSION     AU132868.1  GI:10993407
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 812)
  AUTHORS   Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Yamamoto,J.,
            Nishikawa,T., Nakamura,Y., Nagai,T., Sugano,S., Masuho,Y. and
            Isogai,T.
  TITLE     HRI human cDNA project (Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y.,
            Saito,K., Yamamoto,J., Nishikawa,T., Nakamura,Y., Nagai,T., Sugano
            ,S., Masuho,Y., Isogai,T.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Takao Isogai
            Genomics Laboratory
            Helix Research Institute
            1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            Tel: 81-438-52-3951
            Fax: 81-438-52-3952
            Email: genomics@hri.co.jp
            HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
            Research Institute; cDNA library construction: Department of
            Virology, Institute of Medical Science, University of Tokyo, and
            Helix Research Institute.
FEATURES             Location/Qualifiers
     source          1. .812
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                     /db_xref="taxon:9606"
                     /clone="NT2RP4000750"
                     /clone_lib="NT2RP4"
                     /cell_type="teratocarcinoma"
                     /cell_line="NT2"
                     /note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor
                     cells after 2-weeks retinoic acid (RA) induction"
BASE COUNT      193 a    226 c    241 g    152 t
ORIGIN
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  Best Local Similarity   99.3%;  Pred. No. 5.1e-174;
  Matches  712;  Conservative    0;  Mismatches    3;  Indels    2;  Gaps    2;

Qy      1 cacacagcctactttccaagcggagccatgtctggtaacggcaatgcggctgcaacggcg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     97 CACACAGCCTACTTTCCAAGCGGAGCCATGTCTGGTAACGGCAATGCGGCTGCAACGGCG 156

Qy     61 gaagaaaacagcccaaagatgagagtgattcgcgtgggtacccgcaagagccagcttgct 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    157 GAAGAAAACAGCCCAAAGATGAGAGTGATTCGCGTGGGTACCCGCAAGAGCCAGCTTGCT 216

Qy    121 cgcatacagacggacagtgtggtggcaacattgaaagcctcgtaccctggcctgcagttt 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    217 CGCATACAGACGGACAGTGTGGTGGCAACATTGAAAGCCTCGTACCCTGGCCTGCAGTTT 276

Qy    181 gaaatcattgctatgtccaccacaggggacaagattcttgatactgcactctctaagatt 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    277 GAAATCATTGCTATGTCCACCACAGGGGACAAGATTCTTGATACTGCACTCTCTAAGATT 336

Qy    241 ggagagaaaagcctgtttaccaaggagcttgaacatgccctggagaagaatgaagtggac 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    337 GGAGAGAAAAGCCTGTTTACCAAGGAGCTTGAACATGCCCTGGAGAAGAATGAAGTGGAC 396

Qy    301 ctggttgttcactccttgaaggacctgcccactgtgcttcctcctggcttcaccatcgga 360
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Db    397 CTGGTTGTTCACTCCTTGAAGGACCTGCCCACTGTGCTTCCTCCTGACTTCACCATCGGA 456

Qy    361 gccatctgcaagcgggaaaaccctcatgatgctgttgtctttcacccaaaatttgttggg 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    457 GCCATCTGCAAGCGGGAAAACCCTCATGATGCTGTTGTCTTTCACCCAAAATTTGTTGGG 516

Qy    421 aagaccctagaaaccctgccagagaagagtgtggtgggaaccagctccctgcgaagagca 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    517 AAGACCCTAGAAACCCTGCCAGAGAAGAGTGTGGTGGGAACCAGCTCCCTGCGAAGAGCA 576

Qy    481 gcccagctgcagagaaagttcccgcatctggagttcaggagtattcggggaaacctcaac 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    577 GCCCAGCTGCAGAGAAAGTTCCCGCATCTGGAGTTCAGGAGTATTCGGGGAAACCTCAAC 636

Qy    541 acccggcttcggaagctggacgagcagcaggagttcagtgccatcatcctggcaacagct 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    637 ACCCGGCTTCGGAAGCTGGACGAGCAGCAGGAGTTCAGTGCCATCATCCTGGCAACAGCT 696

Qy    601 ggcctgcagcgcatgggctggcacaaccgggt-tgggcagatcctgcaccctgaggaatg 659
          |||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db    697 GGCCTGCAGCGCATGGGCTGGCACAACCGGGTGGGGGCAGATCCTGCACCCTGAGGAATG 756

Qy    660 catgtatgctgtgggccaggggccttgggcgtggaagtgcgagccaaggaccagga 716
          |||||||||||||||||||||||||||||||| ||||| ||||||||||||||
Db    757 CATGTATGCTGTGGGCCAGGGGCCTTGGGCGTGGAA-TGCGAACCAAGGACCAGGA 812
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RESULT  10
AL579416/c
LOCUS       AL579416      838 bp    mRNA            EST       16-FEB-2001
DEFINITION  AL579416 LTI_FL012_TC1 Homo sapiens cDNA clone CS0DH004YP13 3 prime
            , mRNA sequence.
ACCESSION   AL579416
VERSION     AL579416.1  GI:12944439
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 838)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .838
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DH004YP13"
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                     /clone_lib="LTI_FL012_TC1"
                     /tissue_type="T cells from T cell leukemia"
                     /lab_host="DH10B"
                     /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-stranded cDNA was digested with Not I and cloned
                     into the Not I and Eco RV sites of the pCMVSPORT 6 vector.
                     Library was constructed by Life Technologies. Contact :
                     Feng Liang Life Technologies, a division of Invitrogen
                     9800 Medical Center Drive Rockville, Maryland 20850, USA
                     Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT       160 a    243 c    225 g    189 t     21 others
ORIGIN


  Query Match             61.3%;  Score 682;  DB 106;  Length 838;
  Best Local Similarity   95.4%;  Pred. No. 2.4e-172;
  Matches  702;  Conservative   18;  Mismatches   14;  Indels    2;  Gaps    2;

Qy    378 aaaccctcatgatgctgttgtctttcacccaaaatttgttgggaagaccctagaaaccct 437
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Db    838 AAACCCTCATGATGCTKTTGTCTTTCACCCAAAATTTGTT-GGAAGACCCTAGAAACCCT 780

Qy    438 gccagagaagagtgtggtgggaaccagctccctgcgaagagcagcccagctgcagagaaa 497
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    779 GCCAGAGAAGAGTGTGGTGGGAACCAGCTCCCTGCGAAGAGCAGCCCAGCTGCAGAGAAA 720

Qy    498 gttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttcggaagct 557
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    719 GTTCCCGCATCTGGAGTTCAGGAGTATTCGGGGAAACCTCAACACCCGGCTTCGGAAGCT 660

Qy    558 ggacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatggg 617
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    659 GGACGAGCAGCAGGAGTTCAGTGCCATCATCCTGGCAACAGCTGGCCTGCAGCGCATGGG 600

Qy    618 ctggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctgtgggcca 677
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    599 CTGGCACAACCGGGTGGGGCAGATCCTGCACCCTGAGGAATGCATGTATGCTGTGGGCCA 540

Qy    678 gggggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgt 737
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    539 GGGGGCCTTGGGCGTGGAAGTGCGAGCCAAGGACCAGGACATCTTGGATCTGGTGGGTGT 480

Qy    738 gctgcacgatcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacct 797
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    479 GCTGCACGATCCCGAGACTCT-CTTCGCTGCATCGCTGAAAGGGCCTTCCTGAGGCACCT 421

Qy    798 ggaaggaggctgcagtgtgccagtagccgtgcatacagctatgaaggatgggcaactgta 857
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420 GGAAGGAGGCTGCAGTGTGCCAGTAGCCGTGCATACAGCTATGAAGGATGGGCAACTGTA 361

Qy    858 cctgactggaggagtctggagtctagacggctcagatagcatacaagagaccatgcaggc 917
          ||| |||||||||:|||||||||||||||:|| |||||:|||||||||||:||||||||||
Db    360 CCTCACTGGAGGASTCTGGAGTCTAGACSGCCCAGATMGCATACAAGAGMCCATGCAGGC 301

Qy    918 taccatccatgtccctgcccagcatgaagatggccctgaggatgacccacagttggtagg 977
          ||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||:|
Db    300 TACCATCCATGTCCCTSCCCAGCATGAAGATGGCCCTGAGGATGACCCACAGTTGGTASG 241

Qy    978 catcactgctcgtaacattccacgagggccccagttggctgcccagaacttgggcatcag 1037
          ||||||:||:|||:|||||||||||||||||||||||||||||||:||||||||||||
Db    240 CATCACYGCYCGTMACATTCCACGAGGGCCCCAGTTGGCTGCCCARAACTTGGGCATCTM 181

Qy   1038 cctggccaacttgttgctgagcaaaggagccaaaaacatcctggatgttgcacggcaattt 1097
          |||||||||:  :| ||||| :|||||| : |||||||||||||||:||||||||  |
Db    180 CCTGGCCAAMAARTAGCTGAAMAAAGGAAMAAAAAACATCCTGGATGTDGCACGGCAGCT 121

Qy   1098 gaacgatgcccattaa 1113
           |||||||||:|||:|
Db    120 TAACGATGCCSATTRA 105
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RESULT  11
BE547860
LOCUS       BE547860      804 bp    mRNA            EST       09-AUG-2000
DEFINITION  601074758F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3460575 5',
            mRNA sequence.
ACCESSION   BE547860
VERSION     BE547860.1  GI:9776505
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 804)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Incyte Genomics, Inc.
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM8455  row: d  column: 16
            High quality sequence stop: 670.
FEATURES             Location/Qualifiers
     source          1. .804
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3460575"
                     /clone_lib="NIH_MGC_12"
                     /tissue_type="cervical carcinoma cell line"
                     /lab_host="DH10B"
                     /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.4 kb. Library prepared by Life
                     Technologies."
BASE COUNT      171 a    226 c    235 g    172 t
ORIGIN


  Query Match             60.3%;  Score 671.4;  DB 137;  Length 804;
  Best Local Similarity   94.0%;  Pred. No. 1.7e-169;
  Matches  742;  Conservative    0;  Mismatches   41;  Indels    6;  Gaps    4;

Qy     86 tgattcgcgtgggtacccgcaagagccagcttgctcgcatacagacggacagtgtggtgg 145
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TGATTCGCGTGGGTACCCGCAAGAGCCAGCTTGCTCGCATACAGACGGACAGTGTGGTGG 60

Qy    146 caacattgaaagcctcgtaccctggcctgcagtttgaaatcattgctatgtccaccacag 205
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CAACATTGAAAGCCTCGTACCCTGGCCTGCAGTTTGAAATCATTGCTATGTCCACCACAG 120

Qy    206 gggacaagattcttgatactgcactctctaagattggagagaaaagcctgtttaccaagg 265
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GGGACAAGATTCTTGATACTGCACTCTCTAAGATTGGAGAGAAAAGCCTGTTTACCAAGG 180

Qy    266 agcttgaacatgccctggagaagaatgaagtggacctggttgttcactccttgaaggacc 325
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AGCTTGAACATGCCCTGGAGAAGAATGAAGTGGACCTGGTTGTTCACTCCTTGAAGGACC 240

Qy    326 tgcccactgtgcttcctcctggcttcaccatcggagccatctgcaagcgggaaaaccctc 385
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TGCCCACTGTGCTTCCTCCTGGCTTCACCATCGGAGCCATCTGCAAGCGGGAAAACCCTC 300

Qy    386 atgatgctgttgtctttcacccaaaatttgttgggaagaccctagaaaccctgccagaga 445
          |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db    301 ATGATGCTGTTGTCTTTCACCCAAAATTCGTTGGGAAGACCCTAGAAACCCTGCCAGAGA 360

Qy    446 agagtgtggtgggaaccagctccctgcgaagagcagcccagctgcagagaaagttcccgc 505
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Db    361 AGAGTGTGGTGGGAACCAGCTCCCTGCGAAGAGCAGCCCAGCTGCAGAGAAAGTTCCCGC 420

Qy    506 atctggagttcaggagtattcggggaaacctcaacacccggcttcggaagctggacgagc 565
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ATCTGGAGTTCAGGAGTATTCGGGGAAACCTCAACACCCGGCTTCGGAAGCTGGACGAGC 480

Qy    566 agcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatgggctggcaca 625
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AGCAGGAGTTCAGTGCCATCATCCTGGCAACAGCTGGCCTGCAGCGCATGGGCTGGCACA 540

Qy    626 accgggttgggcagatcctgcaccctgaggaatgcatgtatgctgtgggccaggggggcct 685
          ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ACCGGGTGGGGCAGATCCTGCACCCTGAGGAATGCATGTATGCTGTGGGCCAGGGGGCCT 600

Qy    686 tgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtgctgcacg 745
          | |||||||||||||||||| || ||||||||||||||||||||||||||||||||||||
Db    601 TCGGCGTGGAAGTGCGAGCCACGGCCCAGGACATCTTGGATCTGGTGGGTGTGCTGCACG 660

Qy    746 atcccgagactctg--cttcgctgcatcgctga--aagggccttcctgaggcacctggaa 801
          ||||||||||||||    |    |||||||||  |  | ||||  ||||||||||||||||||
Db    661 ATCCCGAGACTCTGGCTTCGCTTGCATCGCTTACTAGGGGCTTTCCTGAGGCACCTGGAA 720

Qy    802 -ggaggctgcagtgt-gccagtagccgtgcatacagctatgaaggatgggcaactgtacc 859
           || |||||  ||| ||| ||| |||| | | | ||       | || |   |||  ||
Db    721 CCGATGCTGCGTTGTGGCCCGTATCCGTTCCTTCCGCCTCTCCCGCTGCGTCCCTGGTCC 780

Qy    860 tgactggag 868
          ||   | ||
Db    781 TGCTGGCAG 789


RESULT 12
AL520284/c
LOCUS       AL520284      919 bp    mRNA            EST       13-FEB-2001
DEFINITION  AL520284 LTI_NFL004_NBC2 Homo sapiens cDNA clone CS0DB006YG07 3
            prime, mRNA sequence.
ACCESSION   AL520284
VERSION     AL520284.1  GI:12783777
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 919)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .919
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DB006YG07"
                     /clone_lib="LTI_NFL004_NBC2"
                     /sex="male"
                     /tissue_type="neuroblastoma cells"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector.  Library was normalized. Library was constructed
                     by Life Technologies.  Contact : Feng Liang Life
                     Technologies, a division of Invitrogen 9800 Medical Center
                     Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
                     8371 Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      191 a    276 c    248 g    202 t      2 others
ORIGIN
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  Query Match           59.2%;  Score 659.2;  DB 105;  Length 919;
  Best Local Similarity   98.7%;  Pred. No. 3.2e-166;
  Matches  705;  Conservative    1;  Mismatches    4;  Indels    4;  Gaps    4;

Qy    400 tttcacccaaaatttgttgggaagaccctagaaaccctgccagagaagagtgtggtggga 459
          :|||||||||||||||| |||||||||||||||||||||||||||||||||||||| |||
Db    918 YTTCACCCAAAATTTGTT-GGAAGACCCTAGAAACCCTGCCAGAGAAGAGTGTGGT-GGA 861

Qy    460 accagctccctgcgaagagcagcccagctgcagagaaagttcccgcatctggagttcagg 519
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    860 ACCAGCTCCCTGCGAAGAGCAGCCCAGCTGCAGAGAAAGTTCCCGCATCTGGAGTTCAGG 801

Qy    520 agtattcggggaaacctcaacacccggcttcggaagctggacgagcagcaggagttcagt 579
          ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    800 AGTATTC-GGGAAACCTCAACACCCGGCTTCGGAAGCTGGACGAGCAGCAGGAGTTCAGT 742

Qy    580 gccatcatcctggcaacagctggcctgcagcgcatgggctggcacaaccgggttgggcag 639
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db    741 GCCATCATCCTGGCAACAGCTGGCCTGCAGCGCATGGGCTGGCACAACCGGGTGGGGCAG 682

Qy    640 atcctgcaccctgaggaatgcatgtatgctgtgggccaggggggccttgggcgtggaagtg 699
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    681 ATCCTGCACCCTGAGGAATGCATGTATGCTGTGGGCCAGGGGGCCTTGGGCGTGGAAGTG 622

Qy    700 cgagccaaggaccaggacatcttggatctggtgggtgtgctgcacgatcccgagactctg 759
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    621 CGAGCCAAGGACCAGGACATCTTGGATCTGGTGGGTGTGCTGCACGATCCCGAGACTCT- 561

Qy    760 cttcgctgcatcgctgaaagggccttcctgaggcacctggaaggaggctgcagtgtgcca 819
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    562 CTTCGCTGCATCGCTGAAAGGGCCTTCCTGAGGCACCTGGAAGGAGGCTGCAGTGTGCCA 503

Qy    820 gtagccgtgcatacagctatgaaggatgggcaactgtacctgactggaggagtctggagt 879
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Db    502 GTAGCCGTGCATACAGCTATGAAGGATGGGCAACTGTACCTGACTGGAGGAGTCTGGAGT 443

Qy    880 ctagacggctcagatagcatacaagagaccatgcaggctaccatccatgtccctgcccag 939
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Db    442 CTAGACGGCTCAGATAGCATACAAGAGACCATGCAGGCTACCATCCATGTCCCTGCCCAG 383

Qy    940 catgaagatggccctgaggatgacccacagttggtaggcatcactgctcgtaacattcca 999
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    382 CATGAAGATGGCCCTGAGGATGACCCACAGTTGGTAGGCATCACTGCTCGTAACATTCCA 323

Qy   1000 cgagggccccagttggctgcccagaacttgggcatcagcctggccaacttgttgctgagc 1059
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    322 CGAGGGCCCCAGTTGGCTGCCCAGAACTTGGGCATCAGCCTGGCCAACTTGTTGCTGAGC 263

Qy   1060 aaaggagccaaaaacatcctggatgttgcacggcaattgaacgatgcccattaa 1113
          |||||||||||||||||||||||||||||||||  | ||||||||||||||||
Db    262 AAAGGAGCCAAAAACATCCTGGATGTTGCACGGCAGCTTAACGATGCCCATTAA 209


RESULT 13
BE561038
LOCUS       BE561038     1087 bp    mRNA            EST       15-AUG-2000
DEFINITION  601344655F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677748 5',
            mRNA sequence.
ACCESSION   BE561038
VERSION     BE561038.1  GI:9804758
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1087)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
```

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            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
           Plate: LLCM353  row: m  column: 13
           High quality sequence stop: 723.
FEATURES             Location/Qualifiers
     source          1. .1087
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:3677748"
                     /clone_lib="NIH_MGC_8"
                     /tissue_type="Burkitt lymphoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      270 a    291 c    345 g    181 t
ORIGIN


  Query Match             59.1%;  Score 657.8;  DB 137;  Length 1087;
  Best Local Similarity   92.4%;  Pred. No. 8e-166;
  Matches  725;  Conservative    0;  Mismatches   57;  Indels    3;  Gaps    3;

Qy       1 cacacagcctactttccaagcggagccatgtctggtaacggcaatgcggctgcaacggcg 60
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Db      83 CACACAGCCTACTTTCCAAGCGGAGCCATGTCTGGTAACGGCAATGCGGCTGCAACGGCG 142

Qy      61 gaagaaaacagcccaaagatgagagtgattcgcgtgggtacccgcaagagccagcttgct 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     143 GAAGAAAACAGCCCAAAGATGAGAGTGATTCGCGTGGGTACCCGCAAGAGCCAGCTTGCT 202

Qy     121 cgcatacagacggacagtgtggtggcaacattgaaagcctcgtaccctggcctgcagttt 180
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Db     203 CGCATACAGACGGACAGTGTGGTGGCAACATTGAAAGCCTCGTACCCTGGCCTGCAGTTT 262

Qy     181 gaaatcattgctatgtccaccacaggggacaagattcttgatactgcactctctaagatt 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     263 GAAATCATTGCTATGTCCACCACAGGGGACAAGATTCTTGATACTGCACTCTCTAAGATT 322

Qy     241 ggagagaaaagcctgtttaccaaggagcttgaacatgccctggagaagaatgaagtggac 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     323 GGAGAGAAAAGCCTGTTTACCAAGGAGCTTGAACATGCCCTGGAGAAGAATGAAGTGGAC 382

Qy     301 ctggttgttcactccttgaaggacctgcccactgtgcttcctcctggcttcaccatcgga 360
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Db     383 CTGGTTGTTCACTCCTTGAAGGACCTGCCCACTGTGCTTCCTCCTGGCTTCACCATCGGA 442

Qy     361 gccatctgcaagcgggaaaaccctcatgatgctgttgtctttcacccaaaatttgttggg 420
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Db     443 GCCATCTGCAAGCGGGAAAACCCTCATGATGCTGTTGTCTTTCACCCAAAATTTGTTGGG 502

Qy     421 aagaccctagaaaccctgccagagaagagtgtggtgggaaccagctccctgcgaagagca 480
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Db     503 AAGACCCTAGAAACCCTGCCAGAGAAGAGTGTGGTGGGAACCAGCTCCCTGCGAAGAGCA 562

Qy     481 gcccagctgcagagaaagttcccgcatctggagttcaggagtattcggggaaacctcaac 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     563 GCCCAGCTGCAGAGAAAGTTCCCGCATCTGGAGTTCAGGAGTATTCGGGGAAACCTCAAC 622

Qy     541 acccggcttcggaagctggacgagcagcaggagttc-agtgccatcatcctggcaacagc 599
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db     623 ACCCGGCTTCGGAAGCTGGACGAGCAGCAGGAGTTCAAGTGCCATCATCCTGGCAACAGC 682

Qy     600 tggcctgcagcgcatgggctggcacaaccgggttgggcagatcc-tgcaccctgaggaat 658
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Db     683 TGGGCTGCAGCGCATGGGCTGGCACAACGGGGTGGGGCAGATCCTTGCACACTGAGGAAT 742

Qy     659 gcatgtatgctgtgggccaggggccttgggcgtggaagtgcgagccaaggaccaggaca 718
           |  ||| |||||||||| ||||||||||||||||||         |     |||| |  | |
Db     743 GGCTGTTTGCTGTGGG-CAGGGGGCCTTGGGCGTTTGGAATGGGAGGCAGGAGCCCGGCT 801

Qy     719 tcttggatctggtgggtgtgctgcacgatcccgagactctgcttcgctgcatcgctgaaa 778
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Db     802 TCTGGGTCTGGGGGCGGCGGCGAACCGAGAACCGGTCCGCGGCTCGCTGAAGGGCTCTGA 861

Qy     779 gggcc 783
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Db     862 GGCCC 866


RESULT  14
AL520223
LOCUS       AL520223      908 bp    mRNA            EST       13-FEB-2001
DEFINITION  AL520223 LTI_NFL004_NBC2 Homo sapiens cDNA clone CS0DB006YI03 5
            prime, mRNA sequence.
ACCESSION   AL520223
VERSION     AL520223.1  GI:12783716
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 908)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
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                     /clone="CS0DB006YI03"
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                     /sex="male"
                     /tissue_type="neuroblastoma cells"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector.  Library was normalized. Library was constructed
                     by Life Technologies.  Contact : Feng Liang Life
                     Technologies, a division of Invitrogen 9800 Medical Center
                     Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
                     8371 Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      208 a    245 c    269 g    183 t      3 others
ORIGIN


  Query Match             58.8%;  Score 654.6;  DB 105;  Length 908;
  Best Local Similarity   99.3%;  Pred. No. 5.5e-165;
  Matches  676;  Conservative    2;  Mismatches    1;  Indels    2;  Gaps    2;

Qy      60 ggaagaaaacagcccaaagatgagagtgattcgcgtgggtacccgcaagagccagcttgc 119
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Qy     120 tcgcatacagacggacagtgtggtggcaacattgaaagcctcgtaccctggcctgcagtt 179
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Db     290 TCGCATACAGACGGACAGTGTGGTGGCAACATTGAAAGCCTCGTACCCTGGCCTGCAGTT 349

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Qy    420 gaagaccctagaaaccctgccagagaagagtgtggtgggaaccagctccctgcgaagagc 479
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Db    590 GAAGACCCTAGAAACCCTGCCAGAGAAGAGTGTGGTGGGAA-CAGCTCCCTGCGAAGAGC 648

Qy    480 agcccagctgcagagaaagttcccgcatctggagttcaggagtattcggggaaacctcaa 539
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LOCUS       BF971877      970 bp    mRNA            EST       22-JAN-2001
DEFINITION  602240467F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4328848 5',
            mRNA sequence.
ACCESSION   BF971877
VERSION     BF971877.1  GI:12339092
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 970)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1189  row: f  column: 17
            High quality sequence stop: 724.
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     source          1. .970
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                     /db_xref="taxon:9606"
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                     /note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using  ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."
BASE COUNT      244 a    262 c    296 g    168 t
ORIGIN
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  Best Local Similarity   94.8%;  Pred. No. 5.2e-164;
  Matches  716;  Conservative    0;  Mismatches   35;  Indels    4;  Gaps    4;

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Qy    181 gaaatcattgctatgtccaccacaggggacaagattcttgatactgcactctctaagatt 240
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Qy    241 ggagagaaaagcctgtttaccaaggagcttgaacatgccctggagaagaatgaagtggac 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    481 gcccagctgcagagaaagttcccgcatctggagttcaggagtattcggggaaacctcaac 540
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Db    590 G-CCAGCTGCAGAGAAAGTTCCCGCATCTGGAGTTCAGGAGTATCCGGGGAAACCTCAAC 648

Qy    541 acccggcttcggaagctggacgagcagcaggagttcagtgccatcatcctggcaa-cagc 599
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Db    649 ACCCGGCTTCGGAAGCTGGACGAGCAGCAGGAGTTCAGTGCCATCATCCTGGCAACCAGG 708

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Qy    720 cttggatctggtgggtgtgctgcacgatcccgaga 754
          |||| | | |||        |||| ||||| |
Db    827 TTTGGGACACGCGGGGAGTGCTGACGAACCCGAAA 861
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: October 6, 2001, 17:39:53 ; Search time 90.47 Seconds
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2328.985 Million cell updates/sec

Title: US-09-601-138-12
Perfect score: 1113
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Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	36.2	3.3	290	1	US-08-030-731A-41	Sequence 41, Appl
c	3	36.2	3.3	290	1	US-08-030-731A-42	Sequence 42, Appl
	4	36.2	3.3	304	1	US-07-696-551B-12	Sequence 12, Appl
c	5	35.6	3.2	7218	1	US-08-232-463-14	Sequence 14, Appl
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c	7	34.8	3.1	1889	2	US-08-946-241B-8	Sequence 8, Appli
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c	9	34.8	3.1	1889	3	US-09-309-053-8	Sequence 8, Appli
	10	34.4	3.1	2502	1	US-08-073-384C-7	Sequence 7, Appli
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	16	34.4	3.1	2502	2	US-08-757-653-7	Sequence 7, Appli
	17	34.4	3.1	2502	2	US-08-599-491-7	Sequence 7, Appli
	18	34.4	3.1	2502	2	US-08-756-386-7	Sequence 7, Appli
	19	34.4	3.1	2502	2	US-08-823-516-7	Sequence 7, Appli
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	21	34.4	3.1	2502	3	US-08-759-038-7	Sequence 7, Appli
	22	34.4	3.1	2502	3	US-08-758-314-7	Sequence 7, Appli
	23	34.2	3.1	510	1	US-07-918-953-7	Sequence 7, Appli
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c	42	33	3.0	281	1	US-07-764-655D-13	Sequence 13, Appl
	43	33	3.0	281	6	5514646-1	Patent No. 5514646
	44	33	3.0	3579	1	US-08-674-168-15	Sequence 15, Appl
	45	33	3.0	3579	3	US-08-985-908-18	Sequence 18, Appl

ALIGNMENTS

```
RESULT 1
US-08-599-480-3/c
; Sequence 3, Application US/08599480
; Patent No. 5753459
;  GENERAL INFORMATION:
;    APPLICANT:  Blanco, David R.
;    APPLICANT:  Miller, James N.
;    APPLICANT:  Lovett, Michael A.
;    APPLICANT:  Champion, Cheryl I.
;    APPLICANT:  Tempst, Paul J.
;    TITLE OF INVENTION:  NUCLEOTIDE AND AMINO ACID SEQUENCES OF A
;    TITLE OF INVENTION:  T. Pallidum RARE OUTER MEMBRANE PROTEIN
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/599,480
;      FILING DATE:  23-JAN-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Learn, June M.
;      REGISTRATION NUMBER:  31,238
;      REFERENCE/DOCKET NUMBER:  07419/018001 (CIP of 016001)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 678-5070
;      TELEFAX:  (619) 678-5099
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  729 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  TROMP2
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..726
US-08-599-480-3
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RESULT   2
US-08-030-731A-41
; Sequence 41, Application US/08030731A
; Patent No. 5426036
;  GENERAL INFORMATION:
;    APPLICANT:  Koller, Klaus-Peter
;    APPLICANT:  Riess, Guenther Johannes
;    APPLICANT:  Uhlmann, Eugen
;    APPLICANT:  Wallmeier, Holger
;    TITLE OF INVENTION:  Processes for the Preparation of Foreign
;    TITLE OF INVENTION:  Proteins in Streptomycetes
;    NUMBER OF SEQUENCES:  48
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W., Suite 700
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/030,731A
;      FILING DATE:  12-MAR-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/189,840
;      FILING DATE:  03-MAY-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/430,622
;      FILING DATE:  01-NOV-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/687,610
;      FILING DATE:  19-APR-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/735,757
;      FILING DATE:  29-JUL-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P 37 14 866.4
;      FILING DATE:  05-MAY-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P 38 37 273.8
;      FILING DATE:  03-NOV-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P 39 27 449.7
;      FILING DATE:  19-AUG-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P 40 12 818.0
;      FILING DATE:  21-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kirschner Michael K.
;      REGISTRATION NUMBER:  34,851
;      REFERENCE/DOCKET NUMBER:  02481-0593-02000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-408-4000
;      TELEFAX:  202-408-4400
;  INFORMATION FOR SEQ ID NO:  41:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  290 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-030-731A-41


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  Matches  116;  Conservative    0;  Mismatches  133;  Indels    0;  Gaps    0;

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RESULT   3
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; Sequence 42, Application US/08030731A
; Patent No. 5426036
;  GENERAL INFORMATION:
;    APPLICANT:  Koller, Klaus-Peter
;    APPLICANT:  Riess, Guenther Johannes
;    APPLICANT:  Uhlmann, Eugen
;    APPLICANT:  Wallmeier, Holger
;    TITLE OF INVENTION:  Processes for the Preparation of Foreign
;    TITLE OF INVENTION:  Proteins in Streptomycetes
;    NUMBER OF SEQUENCES:  48
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W., Suite 700
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/030,731A
;      FILING DATE:  12-MAR-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/189,840
;      FILING DATE:  03-MAY-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/430,622
;      FILING DATE:  01-NOV-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/687,610
;      FILING DATE:  19-APR-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/735,757
;      FILING DATE:  29-JUL-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P 37 14 866.4
;      FILING DATE:  05-MAY-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P 38 37 273.8
;      FILING DATE:  03-NOV-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P 39 27 449.7
;      FILING DATE:  19-AUG-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P 40 12 818.0
;      FILING DATE:  21-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kirschner Michael K.
;      REGISTRATION NUMBER:  34,851
;      REFERENCE/DOCKET NUMBER:  02481-0593-02000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-408-4000
;      TELEFAX:  202-408-4400
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  290 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ANTI-SENSE:  YES
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  5..290
;      OTHER INFORMATION:  /note= "Sequence ID No. 5426036 42 is
;      OTHER INFORMATION:  complementary to Sequence ID No. 5426036 41 at positions
;      OTHER INFORMATION:  5-290 of Sequence ID No. 5426036 41."
US-08-030-731A-42


  Query Match             3.3%;  Score 36.2;  DB 1;  Length 290;
  Best Local Similarity   46.6%;  Pred. No. 0.19;
  Matches  116;  Conservative    0;  Mismatches  133;  Indels    0;  Gaps    0;

Qy    563 agcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatgggctggc 622
          | |||||   || | |  ||  | |  ||| | |      ||||  | ||  ||   |
Db    275 ACCAGCACCTGTGCGGCTCCCACCTAGTGGAAGCTCTCTACCTGGTGTGCGGGGAGCGAG 216

Qy    623 acaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctgtgggccaggggg 682
           |  |      |  |     | ||  |||| |        |   ||||| |||| ||
Db    215 GCTTCTTCTACACACCCAAGACCCGCCGGGAGGCAGAGGACCCTCAGGTGGGGCAGGTGG 156

Qy    683 ccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtgctgc 742
            |||||| ||      | ||      || | |   |||||  |||| |||    ||||
Db    155 AGCTGGGCGGGGGCCCTGGCGCAGGCAGCCTGCAGCCCTTGGCGCTGGAGGGGTCCCTGC 96

Qy    743 acgatcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctggaag 802
          |  | | ||  |   ||   |  |||  | |    |    || |||    || |||||
Db     95 AGAAGCGCGGCATCGTGGAGCAGTGCTGCACCAGCATCTGCTCCCTCTACCAGCTGGAGA 36

Qy    803 gaggctgca 811
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Db     35 ACTACTGCA 27


RESULT   4
US-07-696-551B-12
; Sequence 12, Application US/07696551B
; Patent No. 5232841
;  GENERAL INFORMATION:
;    APPLICANT:  Hashimoto, Tamotsu
;    APPLICANT:  Tsujimura, Atsushi
;    APPLICANT:  Udaka, Shigezo
;    TITLE OF INVENTION:  Process for Preparing Peptide
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W., Suite 700
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  MS-DOS/PC-DOS
;      SOFTWARE:  Patentin Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/696,551B
;      FILING DATE:  19910509
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 2-122166
;      FILING DATE:  11-MAY-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 2-334575
;      FILING DATE:  30-NOV-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lawrence M. Lavin, Jr.
;      REGISTRATION NUMBER:  30,768
;      REFERENCE/DOCKET NUMBER:  2481-1070
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  304 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-696-551B-12


  Query Match             3.3%;  Score 36.2;  DB 1;  Length 304;
  Best Local Similarity   46.6%;  Pred. No. 0.19;
  Matches  116;  Conservative    0;  Mismatches  133;  Indels    0;  Gaps    0;

Qy    563 agcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatgggctggc 622
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Db     43 ACCAGCACCTGTGCGGCTCCCACCTAGTGGAAGCTCTCTACCTGGTGTGCGGGGAGCGAG 102

Qy    623 acaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctgtgggccaggggg 682
           |  |      |  |     | ||  |||| |        |   ||||| |||| ||
Db    103 GCTTCTTCTACACACCCAAGACCCGCCGGGAGGCAGAGGACCCTCAGGTGGGGCAGGTGG 162

Qy    683 ccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtgctgc 742
            |||||| ||      | ||      || | |   |||||  |||| |||    ||||
Db    163 AGCTGGGCGGGGGCCCTGGCGCAGGCAGCCTGCAGCCCTTGGCGCTGGAGGGGTCCCTGC 222

Qy    743 acgatcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctggaag 802
          |  | | ||  |   ||   |  |||  | |    |    || |||    || |||||
Db    223 AGAAGCGCGGCATCGTGGAGCAGTGCTGCACCAGCATCTGCTCCCTCTACCAGCTGGAGA 282
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Qy     803 gaggctgca 811
               |||||
Db     283 ACTACTGCA 291


RESULT   5
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;     APPLICANT:  DORNER, F.
;     APPLICANT:  SCHEIFLINGER, F.
;     APPLICANT:  FALKNER, F. G.
;     TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;     NUMBER OF SEQUENCES:  52
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Foley & Lardner
;       STREET:  1800 Diagonal Road, Suite 500
;       CITY:  Alexandria
;       STATE:  VA
;       COUNTRY:  USA
;       ZIP:  22313-0299
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/232,463
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/935,313
;       FILING DATE:
;       APPLICATION NUMBER:  EP 91 114 300.6
;       FILING DATE:  26-AUG-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  BENT, Stephen A.
;       REGISTRATION NUMBER:  29,768
;       REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (703)836-9300
;       TELEFAX:  (703)683-4109
;       TELEX:  899149
;   INFORMATION FOR SEQ ID NO:  14:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  7218 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     IMMEDIATE SOURCE:
;       CLONE:  pTZgpt-F1s
US-08-232-463-14


  Query Match             3.2%;  Score 35.6;  DB 1;  Length 7218;
  Best Local Similarity   3.3%;  Pred. No. 1.4;
  Matches   11;  Conservative  184;  Mismatches  143;  Indels    0;  Gaps    0;

Qy     418 gggaagaccctagaaaccctgccagagaagagtgtggtgggaaccagctccctgcgaaga 477
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Db    1386 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1327

Qy     478 gcagcccagctgcagagaaagttcccgcatctggagttcaggagtattcggggaaacctc 537
           : ::   ::  : :::::::     : :   ::::   ::::: :   :::::::
Db    1326 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1267

Qy     538 aacacccggcttcggaagctggacgagcagcaggagttcagtgccatcatcctggcaaca 597
           :: :  ::    :::::  ::: ::: :: :::::   :: :  :  :    :: :: :
Db    1266 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1207

Qy     598 gctggcctgcagcgcatgggctggcacaaccgggttgggcagatcctgcaccctgaggaa 657
           :  ::   : :: : : :::  :: : ::  :::  ::: :::    : :    ::::::
Db    1206 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1147

Qy     658 tgcatgtatgctgtgggccaggggccttgggcgtggaagtgcgagccaaggaccaggac 717
           : : : :  : :::  ::::::    ::: : ::::: : :::  :::::  ::::
Db    1146 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1087

Qy     718 atcttggatctggtgggtgtgctgcacgatcccgagac 755
           :    :::   :: ::: :    ||| | ||||  |||
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RESULT   6
US-08-946-241B-1/c
; Sequence 1, Application US/08946241B
; Patent No. 5928941
;  GENERAL INFORMATION:
;     APPLICANT:  Lee, Mu-En
;     APPLICANT:  McA'Nulty, Megan M.
;     TITLE OF INVENTION:  REPRESSOR KRUPPEL-LIKE FACTOR
;     NUMBER OF SEQUENCES:  13
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Fish & Richardson P.C.
;       STREET:  225 Franklin Street
;       CITY:  Boston
;       STATE:  MA
;       COUNTRY:  USA
;       ZIP:  02110-2804
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/946,241B
;       FILING DATE:  07-OCT-1997
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  60/030,035
;       FILING DATE:  05-NOV-1996
;       APPLICATION NUMBER:  60/027,521
;       FILING DATE:  07-OCT-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Creason, Gary L.
;       REGISTRATION NUMBER:  34,310
;       REFERENCE/DOCKET NUMBER:  05433/027001
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-542-5070
;       TELEFAX:  617-542-8906
;       TELEX:  200154
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1889 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     FEATURE:
;       NAME/KEY:  Coding Sequence
;       LOCATION:  434...1843
US-08-946-241B-1


  Query Match             3.1%;  Score 34.8;  DB 2;  Length 1889;
  Best Local Similarity   52.8%;  Pred. No. 1.2;
  Matches   75;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;

Qy     686 tgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtgctgcacg 745
           ||||  ||||||   |    |||   |||| ||   ||    |    | ||  | ||||
Db    1434 TGGGGATGGAAGCCGGGAGGAAGCGGCAGGGCAGGGTGACAGTCCCTGCTGCTCAGCACT 1375

Qy     746 atcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctggaaggag 805
           | | |||| | |  |||  | |  |||  |||   | | |   ||   |||||  |
Db    1374 TCCTCAAGACCCAGGGTCGGGGTAGTCCTGCTGGGGAGCTGCCGCCCCAGGGGGAAGTCG 1315
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Qy    806 gctgcagtgtgccagtagccgt 827
          |||||   ||| || ||| |
Db   1314 TGTGCAGCCGGCCGGTGGCCAT 1293


RESULT   7
US-08-946-241B-8/c
; Sequence 8, Application US/08946241B
; Patent No. 5928941
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Mu-En
;    APPLICANT:  McA'Nulty, Megan M.
;    TITLE OF INVENTION:  REPRESSOR KRUPPEL-LIKE FACTOR
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/946,241B
;      FILING DATE:  07-OCT-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/030,035
;      FILING DATE:  05-NOV-1996
;      APPLICATION NUMBER:  60/027,521
;      FILING DATE:  07-OCT-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Creason, Gary L.
;      REGISTRATION NUMBER:  34,310
;      REFERENCE/DOCKET NUMBER:  05433/027001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-542-5070
;      TELEFAX:  617-542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1889 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  407...1843
US-08-946-241B-8


  Query Match             3.1%;  Score 34.8;  DB 2;  Length 1889;
  Best Local Similarity   52.8%;  Pred. No. 1.2;
  Matches   75;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;

Qy    686 tgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtgctgcacg 745
          ||||  ||||||   |    |||   |||| ||   ||    |    | ||  | ||||
Db   1434 TGGGGATGGAAGCCGGGAGGAAGCGGCAGGGCAGGGTGACAGTCCCTGCTGCTCAGCACT 1375

Qy    746 atcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctggaaggag 805
            | | |||| | |  |||  | |   |||   |||   | | |   ||   |||||  |
Db   1374 TCCTCAAGACCCAGGGTCGGGGTAGTCCTGCTGGGGAGCTGCCGCCCCAGGGGGAAGTCG 1315

Qy    806 gctgcagtgtgccagtagccgt 827
          |||||   ||| || ||| |
Db   1314 TGTGCAGCCGGCCGGTGGCCAT 1293


RESULT   8
US-09-309-053-1/c
; Sequence 1, Application US/09309053
; Patent No. 6077933
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Mu-En
;    APPLICANT:  McA'Nulty, Megan M.
;    TITLE OF INVENTION:  REPRESSOR KRUPPEL-LIKE FACTOR
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/309,053
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/946,241
;      FILING DATE:  07-OCT-1997
;      APPLICATION NUMBER:  60/030,035
;      FILING DATE:  05-NOV-1996
;      APPLICATION NUMBER:  60/027,521
;      FILING DATE:  07-OCT-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Creason, Gary L.
;      REGISTRATION NUMBER:  34,310
;      REFERENCE/DOCKET NUMBER:  05433/027001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-542-5070
;      TELEFAX:  617-542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1889 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  434...1843
US-09-309-053-1


  Query Match             3.1%;  Score 34.8;  DB 3;  Length 1889;
  Best Local Similarity   52.8%;  Pred. No. 1.2;
  Matches   75;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;

Qy    686 tgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtgctgcacg 745
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Db   1434 TGGGGATGGAAGCCGGGAGGAAGCGGCAGGGCAGGGTGACAGTCCCTGCTGCTCAGCACT 1375

Qy    746 atcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctggaaggag 805
            | | |||| | |  |||  | |   |||   |||   | | |   ||   |||||  |
Db   1374 TCCTCAAGACCCAGGGTCGGGGTAGTCCTGCTGGGGAGCTGCCGCCCCAGGGGGAAGTCG 1315

Qy    806 gctgcagtgtgccagtagccgt 827
          |||||   ||| || ||| |
Db   1314 TGTGCAGCCGGCCGGTGGCCAT 1293


RESULT   9
US-09-309-053-8/c
; Sequence 8, Application US/09309053
; Patent No. 6077933
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Mu-En
;    APPLICANT:  McA'Nulty, Megan M.
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;    TITLE OF INVENTION:  REPRESSOR KRUPPEL-LIKE FACTOR
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/309,053
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/946,241
;      FILING DATE:  07-OCT-1997
;      APPLICATION NUMBER:  60/030,035
;      FILING DATE:  05-NOV-1996
;      APPLICATION NUMBER:  60/027,521
;      FILING DATE:  07-OCT-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Creason, Gary L.
;      REGISTRATION NUMBER:  34,310
;      REFERENCE/DOCKET NUMBER:  05433/027001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-542-5070
;      TELEFAX:  617-542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1889 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  407...1843
US-09-309-053-8


  Query Match             3.1%;  Score 34.8;  DB 3;  Length 1889;
  Best Local Similarity   52.8%;  Pred. No. 1.2;
  Matches   75;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;

Qy     686 tgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtgctgcacg 745
           ||||  ||||||    |    |||   |||| ||   ||  |    | ||  | ||||
Db    1434 TGGGGATGGAAGCCGGGAGGAAGCGGCAGGGCAGGGTGACAGTCCCTGCTGCTCAGCACT 1375

Qy     746 atcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctggaaggag 805
           | | |||| | |  |||  | |   |||   |||    | | |   ||   |||||  |
Db    1374 TCCTCAAGACCCAGGGTCGGGGTAGTCCTGCTGGGGAGCTGCCGCCCCAGGGGGAAGTCG 1315

Qy     806 gctgcagtgtgccagtagccgt 827
           |||||   ||| || ||| |
Db    1314 TGTGCAGCCGGCCGGTGGCCAT 1293


RESULT  10
US-08-073-384C-7
; Sequence 7, Application US/08073384C
; Patent No. 5541311
;  GENERAL INFORMATION:
;    APPLICANT:  Dahlberg, James E.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Brow, Mary Ann D.
;    TITLE OF INVENTION:  SYNTHESIS-DEFICIENT THERMOSTABLE DNA
;    TITLE OF INVENTION:  POLYMERASE
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HAVERSTOCK, MEDLEN & CARROLL
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/073,384C
;      FILING DATE:  04-JUN-1993
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/986,330
;      FILING DATE:  07-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Carroll, Peter G.
;      REGISTRATION NUMBER:  32,837
;      REFERENCE/DOCKET NUMBER:  FORS-00613
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/705-8410
;      TELEFAX:  415/397-8338
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2502 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-073-384C-7


  Query Match             3.1%;  Score 34.4;  DB 1;  Length 2502;
  Best Local Similarity   44.0%;  Pred. No. 1.8;
  Matches  128;  Conservative    0;  Mismatches  163;  Indels    0;  Gaps    0;

Qy     491 agagaaagttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttc 550
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Db    1232 AGAGGCTCTTCCNGAACCTNNNGCAGCGCCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTT 1291

Qy     551 ggaagctggacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagc 610
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Db    1292 ACCAGGAGGTGGAGAAGCCCCTTTCCCGGGTCCTGGCCCACATGGAGGCCACGGGGGTNC 1351

Qy     611 gcatgggctggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctg 670
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Db    1352 GGCTGGACGTGGCCTACCTCCAGGCCCTNTCCCTGGAGGTGGCGGAGGAGATCCGCCGCC 1411

Qy     671 tgggccaggggggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctgg 730
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Qy     731 tgggtgtgctgcacgatcccgagactctgcttcgctgcatcgctgaaaggg 781
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RESULT  11
US-08-254-359A-7
; Sequence 7, Application US/08254359A
; Patent No. 5614402
;  GENERAL INFORMATION:
;    APPLICANT:  DAHLBERG, JAMES E.
;    APPLICANT:  LYAMICHEV, VICTOR I.
;    APPLICANT:  BROW, MARY ANN D.
;    TITLE OF INVENTION:  5' NUCLEASES DERIVED FROM THERMOSTABLE
;    TITLE OF INVENTION:  DNA POLYMERASE
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HAVERSTOCK, MEDLEN & CARROLL
;      STREET:  220 MONTGOMERY STREET, SUITE 2200
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;       CITY:  SAN FRANCISCO
;       STATE:  CALIFORNIA
;       COUNTRY:  UNITED STATES OF AMERICA
;       ZIP:  94104
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/254,359A
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/073,384
;       FILING DATE:  06-JUN-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/986,330
;       FILING DATE:  07-DEC-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  CARROLL, PETER G.
;       REGISTRATION NUMBER:  32,837
;       REFERENCE/DOCKET NUMBER:  FORS-01000
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 705-8410]
;       TELEFAX:  (415) 397-8338
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2502 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-254-359A-7

  Query Match             3.1%;  Score 34.4;  DB 1;  Length 2502;
  Best Local Similarity   44.0%;  Pred. No. 1.8;
  Matches  128;  Conservative    0;  Mismatches  163;  Indels    0;  Gaps    0;

Qy     491 agagaaagttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttc 550
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Qy     551 ggaagctggacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagc 610
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Qy     611 gcatgggctggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctg 670
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Qy     671 tgggccagggggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctgg 730
           | |   ||| || |||  || |||  | |   ||   |||   ||  |  ||| | |
Db    1412 TCGAGGAGGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCGGGACCAGC 1471

Qy     731 tgggtgtgctgcacgatcccgagactctgcttcgctgcatcgctgaaaggg 781
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RESULT  12
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; Sequence 7, Application US/08483043
; Patent No. 5691142
;  GENERAL INFORMATION:
;    APPLICANT:  Dahlberg, James E.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Brow, Mary Ann D.
;    TITLE OF INVENTION:  SYNTHESIS-DEFICIENT THERMOSTABLE DNA
;    TITLE OF INVENTION:  POLYMERASE
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HAVERSTOCK, MEDLEN & CARROLL
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/483,043
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/073,384
;      FILING DATE:  04-JUN-1993
;      APPLICATION NUMBER:  US 07/986,330
;      FILING DATE:  07-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Carroll, Peter G.
;      REGISTRATION NUMBER:  32,837
;      REFERENCE/DOCKET NUMBER:  FORS-00613
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/705-8410
;      TELEFAX:  415/397-8338
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2502 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-483-043-7

  Query Match             3.1%;  Score 34.4;  DB 1;  Length 2502;
  Best Local Similarity   44.0%;  Pred. No. 1.8;
  Matches  128;  Conservative    0;  Mismatches  163;  Indels    0;  Gaps    0;

Qy     491 agagaaagttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttc 550
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Db    1232 AGAGGCTCTTCCNGAACCTNNNGCAGCGCCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTT 1291

Qy     551 ggaagctggacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagc 610
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Db    1292 ACCAGGAGGTGGAGAAGCCCCTTTCCCGGGTCCTGGCCCACATGGAGGCCACGGGGGTNC 1351

Qy     611 gcatgggctggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctg 670
           |  ||| |  |  | |||     |  |    |||| |    | |||    ||
Db    1352 GGCTGGACGTGGCCTACCTCCAGGCCCTNTCCCTGGAGGTGGCGGAGGAGATCCGCCGCC 1411

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RESULT  13
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; Sequence 7, Application US/08481238
; Patent No. 5795763
;  GENERAL INFORMATION:
;    APPLICANT:  DAHLBERG, JAMES E.
;    APPLICANT:  LYAMICHEV, VICTOR I.
;    APPLICANT:  BROW, MARY ANN D.
;    TITLE OF INVENTION:  SYNTHESIS-DEFICIENT THERMOSTABLE DNA
;    TITLE OF INVENTION:  POLYMERASE
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
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;       ADDRESSEE:  MEDLEN & CARROLL
;       STREET:  220 MONTGOMERY STREET, SUITE 2200
;       CITY:  SAN FRANCISCO
;       STATE:  CALIFORNIA
;       COUNTRY:  USA
;       ZIP:  94104
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/481,238
;       FILING DATE:
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  CARROLL, PETER G.
;       REGISTRATION NUMBER:  32,837
;       REFERENCE/DOCKET NUMBER:  FORS-01798
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 705-8410
;       TELEFAX:  (415) 397-8338
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2502 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-481-238-7


  Query Match             3.1%;  Score 34.4;  DB 1;  Length 2502;
  Best Local Similarity   44.0%;  Pred. No. 1.8;
  Matches  128;  Conservative    0;  Mismatches  163;  Indels    0;  Gaps    0;

Qy     491 agagaaagttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttc 550
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Db    1232 AGAGGCTCTTCCNGAACCTNNNGCAGCGCCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTT 1291

Qy     551 ggaagctggacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagc 610
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Db    1292 ACCAGGAGGTGGAGAAGCCCCTTTCCCGGGTCCTGGCCCACATGGAGGCCACGGGGGTNC 1351

Qy     611 gcatgggctggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctg 670
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Db    1352 GGCTGGACGTGGCCTACCTCCAGGCCCTNTCCCTGGAGGTGGCGGAGGAGATCCGCCGCC 1411

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Db    1412 TCGAGGAGGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCGGGACCAGC 1471

Qy     731 tgggtgtgctgcacgatcccgagactctgcttcgctgcatcgctgaaaggg 781
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; Sequence 7, Application US/08471066B
; Patent No. 5837450
;  GENERAL INFORMATION:
;    APPLICANT:  Dahlberg, James E.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Brow, Mary Ann D.
;    TITLE OF INVENTION:  5' Nucleases Derived From Thermostable
;    TITLE OF INVENTION:  DNA Polyermase
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/471,066B
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/254,359
;      FILING DATE:  06-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/073,384
;      FILING DATE:  04-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/986,330
;      FILING DATE:  07-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  FORS-01800
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2502 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-471-066B-7


  Query Match             3.1%;  Score 34.4;  DB 2;  Length 2502;
  Best Local Similarity   44.0%;  Pred. No. 1.8;
  Matches  128;  Conservative    0;  Mismatches  163;  Indels    0;  Gaps    0;

Qy     491 agagaaagttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttc 550
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Db    1232 AGAGGCTCTTCCNGAACCTNNNGCAGCGCCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTT 1291

Qy     551 ggaagctggacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagc 610
             ||  ||  ||| |||     | | | | | |   ||        ||        |   |
Db    1292 ACCAGGAGGTGGAGAAGCCCCTTTCCCGGGTCCTGGCCCACATGGAGGCCACGGGGGTNC 1351

Qy     611 gcatgggctggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctg 670
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Qy     671 tgggccaggggggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctgg 730
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Db    1412 TCGAGGAGGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCGGGACCAGC 1471

Qy     731 tgggtgtgctgcacgatcccgagactctgcttcgctgcatcgctgaaaggg 781
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Db    1472 TGGAAAGGGTGCTCTTTGACGAGCTNGGGCTTCCCGCCATCGGCAAGACGG 1522


RESULT  15
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; Sequence 7, Application US/08484956
; Patent No. 5843654
;  GENERAL INFORMATION:
;    APPLICANT:  DAHLBERG, JAMES E.
;    APPLICANT:  LYAMICHEV, VICTOR I.
;    APPLICANT:  BROW, MARY ANN D.
;    APPLICANT:  OLDENBURG, MARY C.
;    APPLICANT:  HEISLER, LAURA
;    TITLE OF INVENTION:  DETECTION OF p53 MUTATIONS
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;    NUMBER OF SEQUENCES:  114
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HAVERSTOCK, MEDLEN & CARROLL
;      STREET:  220 MONTGOMERY STREET, SUITE 2200
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,956
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/402,601
;      FILING DATE:  09-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/337,164
;      FILING DATE:  09-NOV-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/254,359
;      FILING DATE:  06-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/073,384
;      FILING DATE:  04-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/986,330
;      FILING DATE:  07-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CARRPOLL ], PETER G.
;      REGISTRATION NUMBER:  32,837
;      REFERENCE/DOCKET NUMBER:  FORS-01801
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2502 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-484-956-7


  Query Match             3.1%;  Score 34.4;  DB 2;  Length 2502;
  Best Local Similarity   44.0%;  Pred. No. 1.8;
  Matches  128;  Conservative    0;  Mismatches  163;  Indels    0;  Gaps    0;

Qy    491 agagaaagttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttc 550
          ||||    |||| | | ||   |    |   |    |||   |      |    |||||
Db   1232 AGAGGCTCTTCCNGAACCTNNNGCAGCGCCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTT 1291

Qy    551 ggaagctggacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagc 610
             ||  ||  ||| |||     | | | | | |   ||        ||      |   |
Db   1292 ACCAGGAGGTGGAGAAGCCCCTTTCCCGGGTCCTGGCCCACATGGAGGCCACGGGGGTNC 1351

Qy    611 gcatgggctggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctg 670
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Db   1352 GGCTGGACGTGGCCTACCTCCAGGCCCTNTCCCTGGAGGTGGCGGAGGAGATCCGCCGCC 1411

Qy    671 tgggccaggggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctgg 730
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Db   1412 TCGAGGAGGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCGGGACCAGC 1471

Qy    731 tgggtgtgctgcacgatcccgagactctgcttcgctgcatcgctgaaaggg 781
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Db   1472 TGGAAAGGGTGCTCTTTGACGAGCTNGGGCTTCCCGCCATCGGCAAGACGG 1522
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Job time: 139 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: October 6, 2001, 17:37:53 ; Search time 162.85 Seconds
(without alignments)
3990.655 Million cell updates/sec

Title: US-09-601-138-1
Perfect score: 1035
Sequence: 1 atgagagtgattcgcgtggg.....aattgaacgatgcccattaa 1035

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	4	1035	100.0	1113	22	AAF72849	Non-erythropoietic
	5	1035	100.0	1260	22	AAF72858	(PDGB) DNA. Homo
c	6	1035	100.0	3988	20	AAX87639	Human porphobilino
c	7	1035	100.0	3988	22	AAF72857	PDGB DNA. Homo sa
	8	1033.4	99.8	1035	20	AAX87632	Human porphobilino
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	10	1033.4	99.8	1035	22	AAF72850	PDGB from spleen.
	11	1033.4	99.8	1035	22	AAF72851	PDGB from bone mar
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	14	1030.2	99.5	1035	20	AAX87638	Human porphobilino
	15	1030.2	99.5	1035	22	AAF72856	PDGB from total br
	16	1030.2	99.5	5446	22	AAF72846	Plasmid pExpl-M2-B
	17	1028.6	99.4	1035	20	AAX87635	Human porphobilino
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	19	1021.4	98.7	1034	20	AAX87634	Human porphobilino
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	22	1021.4	98.7	1034	22	AAF72855	PDGB from total br
	23	160.6	15.5	269223	22	AAF28554	Genomic fragment #
c	24	145.8	14.1	17381	21	AAA81493	N. meningitidis pa
	25	145.8	14.1	349980	21	AAF21607	Neisseria meningit
	26	90	8.7	673	21	AAF11971	Aspergillus oryzae
c	27	89.4	8.6	1689	18	AAV74490	Staphylococcus aur
	28	87.2	8.4	687	21	AAF11990	Aspergillus oryzae
	29	78.4	7.6	681	22	AAF72157	Corynebacterium gl
	30	73.8	7.1	1500	21	AAC42065	Arabidopsis thalia
	31	66	6.4	1149	22	AAA89294	Arabidopsis porpho
	32	64.2	6.2	1020	19	AAX14248	H. pylori GHPO 142
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	36	54.2	5.2	3422	22	AAA89298	Arabidopsis porpho
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c	38	41.6	4.0	765	18	AAT76579	Treponema pallidum
	39	40.8	3.9	10732	21	AAA10594	Gene encoding a su
	40	39.2	3.8	522	22	AAF72154	Corynebacterium gl
	41	39.2	3.8	558	22	AAF72155	Corynebacterium gl
c	42	39.2	3.8	21185	21	AAA63350	Streptomyces globi
c	43	39.2	3.8	63164	21	AAA63348	Streptomyces globi
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ALIGNMENTS

RESULT 1
AAX87630
ID AAX87630 standard; cDNA; 1035 BP.
XX
AC AAX87630;
XX
DT 26-OCT-1999 (first entry)
XX
DE Human porphobilinogen deaminase clone 1.1.
XX
KW Porphobilinogen deaminase; human; haem; ALA deficiency porphyria;
KW porphyria cutanea tarda; hereditary coproporphyria;
KW harderoporphyria; congenital erythropoietic porphyria;
KW variegata porphyria; erythropoietic protoporphyria;
KW hepatoerythropoietic porphyria; acute intermittent porphyria;
KW gene therapy; enzyme replacement therapy; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
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FT variation replace(1020,T)
FT /*tag= e

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PR   30-DEC-1998;   98DK-0001748.
PR   27-JAN-1998;   98DK-0000112.
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PA   (HEME-) HEMEBIOTECH AS.
XX
PI   Fogh J,  Gellerfors P;
XX
DR   WPI; 1999-478987/40.
DR   P-PSDB; AAY06611.
XX
PT   Treatment of acute intermittent porphyria and other porphyric
PT   diseases using an enzyme belonging to the haem biosynthetic pathway
XX
PS   Claim 36; Page 91; 100pp; English.
XX
CC   This is the nucleotide sequence of human PBGD clone 1.1 coding for
CC   an erythropoietic expressed form of porphobilinogen deaminase
CC   (PBGD, see AAY06611).  PBGD catalyses the rate-limiting step of the
CC   haem biosynthetic pathway.  cDNA was cloned from spleen, bone
CC   marrow, lymph node, lung, whole brain and adipose tissue using a
CC   nested PCR strategy.  8 PBGD clones were sequenced (see AAX87630 and
CC   AAX87632-38).  Clone 1.1, from spleen cDNA, has 5 changes from the
CC   previously published sequence but represents the most prevalent
CC   'wild-type' allele in the population.  Mutation of the PBGD gene is
CC   associated with the autosomal dominant disorder acute intermittent
CC   porphyria (AIP).  A claimed method of treating a patient having a
CC   mutation in the PBGD gene comprises using a human PBGD cDNA
CC   sequence of either non-erythropoietic form (see AAX87631) or
CC   erythopoietic form (especially the present sequence) according
CC   to the tissue in which PBGD should be expressed, and transfection
CC   of the patient with the relevant cDNA.  Gene therapy treatment of
CC   patients with AIP by a correction of one of the specific point
CC   mutations identified as causing the disease by use of chimeraplasty
CC   gene repair is also claimed.  Other enzymes involved in the haem
CC   biosynthetic pathway can also be used to treat various porphyrias.
XX
SQ   Sequence 1035 BP; 250 A; 271 C; 302 G; 212 T; 0 other;
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Query Match 100.0%; Score 1035; DB 20; Length 1035;
Best Local Similarity 100.0%; Pred. No. 2e-279;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AC   AAF72848;
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DT   24-APR-2001  (first entry)
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XX
KW   Heme biosynthetic pathway; gene therapy; AIP; ALA;
KW   delta-aminolevulinic acid; deficient porphyria; ADP;
KW   porphyria cutanea tarda; PCT; hereditary coproporphyria; HCP;
KW   harderoporphyria; HDP; variegata porphyria; VP;
KW   congenital erythropoietic porphyria; CEP;
KW   erythropoietic protoporphyria; EPP;
KW   hepatoerythropoietic porphyria; HEP; ds.
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PN   WO200107065-A2.
XX
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PD 01-FEB-2001.
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PR 27-JUL-1999; 99DK-0001071.
PR 19-APR-2000; 2000DK-0000667.
XX
PA (HEME-) HEMEBIOTECH AS.
XX
PI Gellerfors P, Fogh J;
XX
DR WPI; 2001-159639/16.
XX
PT Treatment or prevention of porphyria, by enzyme replacement or gene
PT therapy for correction of mutations, particularly in the
PT porphorbilinogen deaminase gene -
XX
PS Claim 33; Page 200; 207pp; English.
XX
CC The present invention relates to treatment or prevention of a
CC disease caused by deficiency of at least one enzyme of the
CC heme biosynthetic pathway by administering at least one catalyst,
CC optionally combined with gene therapy of the relevant mutation.
CC The invention is useful for treating and/or preventing AIP, ALA
CC (delta-aminolevulinic acid) deficient porphyria (ADP), porphyria
CC cutanea tarda (PCT), hereditary coproporphyria (HCP), harderoporphyria
CC (HDP), variegata porphyria (VP), congenital erythropoietic porphyria
CC (CEP), erythropoietic protoporphyria (EPP) and hepatoerythropoietic
CC porphyria (HEP).
XX
SQ Sequence 1035 BP; 250 A; 271 C; 302 G; 212 T; 0 other;

Query Match 100.0%; Score 1035; DB 22; Length 1035;
Best Local Similarity 100.0%; Pred. No. 2e-279;
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RESULT 3
AAX87631
ID AAX87631 standard; cDNA; 1113 BP.
XX
AC AAX87631;
XX
DT 26-OCT-1999 (first entry)
XX
DE Human non-erythroid porphobilinogen deaminase clone 1.1.1.
XX
KW Porphobilinogen deaminase; human; haem; ALA deficiency porphyria;
KW porphyria cutanea tarda; hereditary coproporphyria;
KW harderoporphyria; congenital erythropoietic porphyria;
KW variegata porphyria; erythropoietic protoporphyria;
KW hepatoerythropoietic porphyria; acute intermittent porphyria;
KW gene therapy; enzyme replacement therapy; ds.
XX
OS Homo sapiens.
XX
PN WO9937325-A2.
XX
PD 29-JUL-1999.
XX
PF 27-JAN-1999; 99WO-DK00040.
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PR 30-DEC-1998; 98DK-0001748.
PR 27-JAN-1998; 98DK-0000112.
XX
PA (HEME-) HEMEBIOTECH AS.
XX
PI Fogh J, Gellerfors P;
XX
DR WPI; 1999-478987/40.
XX
PT Treatment of acute intermittent porphyria and other porphyric
PT diseases using an enzyme belonging to the haem biosynthetic pathway

```
XX
PS   Claim 36; Page 99-100; 100pp; English.
XX
CC   This is the nucleotide sequence of human PBGD clone 1.1.1 coding
CC   for a constitutive form of porphobilinogen deaminase (PBGD).
CC   This enzyme catalyses the third, rate-limiting step of the haem
CC   biosynthetic pathway.  Mutation of the PBGD gene is associated
CC   with the autosomal dominant disorder acute intermittent porphyria
CC   (AIP).  A claimed method of treating a patient having a mutation
CC   in the PBGD gene comprises using a human PBGD cDNA sequence of
CC   either the present, non-erythropoietic form or an erythopoietic
CC   form (see AAX87630) according to the tissue in which PBGD should be
CC   expressed, and transfection of the patient with the relevant cDNA.
CC   Gene therapy treatment of patients with AIP by a correction of one
CC   of the specific point mutations identified as causing the disease
CC   by use of chimeraplasty gene repair is also claimed.  Other enzymes
CC   involved in the haem biosynthetic pathway can also be used to treat
CC   various porphyrias.
XX
SQ   Sequence 1113 BP; 274 A; 294 C; 323 G; 222 T; 0 other;


  Query Match             100.0%;  Score 1035;  DB 20;  Length 1113;
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Qy     421 ttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttcggaagctg 480
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Db     499 ttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttcggaagctg 558

Qy     481 gacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatgggc 540
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Db     559 gacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatgggc 618

Qy     541 tggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctgtgggccag 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     619 tggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctgtgggccag 678

Qy     601 ggggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtg 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     679 ggggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtg 738

Qy     661 ctgcacgatcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctg 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     739 ctgcacgatcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctg 798

Qy     721 gaaggaggctgcagtgtgccagtagccgtgcatacagctatgaaggatgggcaactgtac 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     799 gaaggaggctgcagtgtgccagtagccgtgcatacagctatgaaggatgggcaactgtac 858

Qy     781 ctgactggaggagtctggagtctagacggctcagatagcatacaagagaccatgcaggct 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     859 ctgactggaggagtctggagtctagacggctcagatagcatacaagagaccatgcaggct 918

Qy     841 accatccatgtccctgcccagcatgaagatggccctgaggatgacccacagttggtaggc 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     919 accatccatgtccctgcccagcatgaagatggccctgaggatgacccacagttggtaggc 978

Qy     901 atcactgctcgtaacattccacgagggccccagttggctgcccagaacttgggcatcagc 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     979 atcactgctcgtaacattccacgagggccccagttggctgcccagaacttgggcatcagc 1038

Qy     961 ctggccaacttgttgctgagcaaaggagccaaaaacatcctggatgttgcacggcaattg 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1039 ctggccaacttgttgctgagcaaaggagccaaaaacatcctggatgttgcacggcaattg 1098

Qy    1021 aacgatgcccattaa 1035
          ||||||||||||||||
Db    1099 aacgatgcccattaa 1113


RESULT   4
AAF72849
ID   AAF72849 standard; DNA; 1113 BP.
XX
AC   AAF72849;
XX
DT   24-APR-2001  (first entry)
XX
DE   Non-erythropoietic form PBGD 1.2.
XX
KW   Heme biosynthetic pathway; gene therapy; AIP; ALA;
KW   delta-aminolevulinic acid; deficient porphyria; ADP;
KW   porphyria cutanea tarda; PCT; hereditary coproporphyria; HCP;
KW   harderoporphyria; HDP; variegata porphyria; VP;
KW   congenital erythropoietic porphyria; CEP;
KW   erythropoietic protoporphyria; EPP;
KW   hepatoerythropoietic porphyria; HEP; ds.
XX
OS   Homo sapiens.
XX
PN   WO200107065-A2.
XX
PD   01-FEB-2001.
XX
PF   27-JUL-2000; 2000WO-DK00425.
XX
PR   27-JUL-1999;   99DK-0001071.
PR   19-APR-2000; 2000DK-0000667.
XX
PA   (HEME-) HEMEBIOTECH AS.
XX
PI   Gellerfors P,  Fogh J;
XX
DR   WPI; 2001-159639/16.
XX
PT   Treatment or prevention of porphyria, by enzyme replacement or gene
PT   therapy for correction of mutations, particularly in the
PT   porphorbilinogen deaminase gene  -
XX
PS   Claim 33; Page 200; 207pp; English.
XX
CC   The present invention relates to treatment or prevention of a
CC   disease caused by deficiency of at least one enzyme of the
CC   heme biosynthetic pathway by administering at least one catalyst,
CC   optionally combined with gene therapy of the relevant mutation.
CC   The invention is useful for treating and/or preventing AIP, ALA
CC   (delta-aminolevulinic acid) deficient porphyria (ADP), porphyria
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CC   cutanea tarda (PCT), hereditary coproporphyria (HCP), harderoporphyria
CC   (HDP), variegata porphyria (VP), congenital erythropoietic porphyria
CC   (CEP ), erythropoietic protoporphyria (EPP) and hepatoerythropoietic
CC   porphyria (HEP).
XX
SQ   Sequence 1113 BP; 274 A; 294 C; 323 G; 222 T; 0 other;


  Query Match            100.0%;  Score 1035;  DB 22;  Length 1113;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-279;
  Matches 1035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 atgagagtgattcgcgtgggtacccgcaagagccagcttgctcgcatacagacggacagt 60
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Db     79 atgagagtgattcgcgtgggtacccgcaagagccagcttgctcgcatacagacggacagt 138

Qy     61 gtggtggcaacattgaaagcctcgtaccctggcctgcagtttgaaatcattgctatgtcc 120
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Db    139 gtggtggcaacattgaaagcctcgtaccctggcctgcagtttgaaatcattgctatgtcc 198

Qy    121 accacaggggacaagattcttgatactgcactctctaagattggagagaaaagcctgttt 180
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Db    199 accacaggggacaagattcttgatactgcactctctaagattggagagaaaagcctgttt 258

Qy    181 accaaggagcttgaacatgccctggagaagaatgaagtggacctggttgttcactccttg 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    259 accaaggagcttgaacatgccctggagaagaatgaagtggacctggttgttcactccttg 318

Qy    241 aaggacctgcccactgtgcttcctcctggcttcaccatcggagccatctgcaagcgggaa 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    319 aaggacctgcccactgtgcttcctcctggcttcaccatcggagccatctgcaagcgggaa 378

Qy    301 aaccctcatgatgctgttgtctttcacccaaaatttgttgggaagaccctagaaaccctg 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    379 aaccctcatgatgctgttgtctttcacccaaaatttgttgggaagaccctagaaaccctg 438

Qy    361 ccagagaagagtgtggtgggaaccagctccctgcgaagagcagcccagctgcagagaaag 420
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Db    439 ccagagaagagtgtggtgggaaccagctccctgcgaagagcagcccagctgcagagaaag 498

Qy    421 ttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttcggaagctg 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    499 ttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttcggaagctg 558

Qy    481 gacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatgggc 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    559 gacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatgggc 618

Qy    541 tggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctgtgggccag 600
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Db    619 tggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctgtgggccag 678

Qy    601 ggggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtg 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    679 ggggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtg 738

Qy    661 ctgcacgatcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctg 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    739 ctgcacgatcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctg 798

Qy    721 gaaggaggctgcagtgtgccagtagccgtgcatacagctatgaaggatgggcaactgtac 780
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Qy    781 ctgactggaggagtctggagtctagacggctcagatagcatacaagagaccatgcaggct 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    859 ctgactggaggagtctggagtctagacggctcagatagcatacaagagaccatgcaggct 918

Qy    841 accatccatgtccctgcccagcatgaagatggccctgaggatgacccacagttggtaggc 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    919 accatccatgtccctgcccagcatgaagatggccctgaggatgacccacagttggtaggc 978

Qy    901 atcactgctcgtaacattccacgagggccccagttggctgcccagaacttgggcatcagc 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    979 atcactgctcgtaacattccacgagggccccagttggctgcccagaacttgggcatcagc 1038

Qy    961 ctggccaacttgttgctgagcaaaggagccaaaaacatcctggatgttgcacggcaattg 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1039 ctggccaacttgttgctgagcaaaggagccaaaaacatcctggatgttgcacggcaattg 1098

Qy   1021 aacgatgcccattaa 1035
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Db   1099 aacgatgcccattaa 1113


RESULT   5
AAF72858
ID   AAF72858 standard; DNA; 1260 BP.
XX
AC   AAF72858;
XX
DT   24-APR-2001  (first entry)
XX
DE   (PDGB) DNA.
XX
KW   Heme biosynthetic pathway; gene therapy; AIP; ALA;
KW   delta-aminolevulinic acid; deficient porphyria; ADP;
KW   porphyria cutanea tarda; PCT; hereditary coproporphyria; HCP;
KW   harderoporphyria; HDP; variegata porphyria; VP;
KW   congenital erythropoietic porphyria; CEP;
KW   erythropoietic protoporphyria; EPP;
KW   hepatoerythropoietic porphyria; HEP; ds.
XX
OS   Homo sapiens.
XX
PN   WO200107065-A2.
XX
PD   01-FEB-2001.
XX
PF   27-JUL-2000; 2000WO-DK00425.
XX
PR   27-JUL-1999;   99DK-0001071.
PR   19-APR-2000; 2000DK-0000667.
XX
PA   (HEME-) HEMEBIOTECH AS.
XX
PI   Gellerfors P,  Fogh J;
XX
DR   WPI; 2001-159639/16.
XX
PT   Treatment or prevention of porphyria, by enzyme replacement or gene
PT   therapy for correction of mutations, particularly in the
PT   porphorbilinogen deaminase gene
XX
PS   Disclosure; Page 205; 207pp; English.
XX
CC   The present invention relates to treatment or prevention of a
CC   disease caused by deficiency of at least one enzyme of the
CC   heme biosynthetic pathway by administering at least one catalyst,
CC   optionally combined with gene therapy of the relevant mutation.
CC   The invention is useful for treating and/or preventing AIP, ALA
CC   (delta-aminolevulinic acid) deficient porphyria (ADP), porphyria
CC   cutanea tarda (PCT), hereditary coproporphyria (HCP), harderoporphyria
CC   (HDP), variegata porphyria (VP), congenital erythropoietic porphyria
CC   (CEP ), erythropoietic protoporphyria (EPP) and hepatoerythropoietic
CC   porphyria (HEP).
XX
SQ   Sequence 1260 BP; 309 A; 335 C; 358 G; 258 T; 0 other;


  Query Match            100.0%;  Score 1035;  DB 22;  Length 1260;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-279;
  Matches 1035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db    131 atgagagtgattcgcgtgggtacccgcaagagccagcttgctcgcatacagacggacagt 190

Qy     61 gtggtggcaacattgaaagcctcgtaccctggcctgcagtttgaaatcattgctatgtcc 120
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Qy    121 accacaggggacaagattcttgatactgcactctctaagattggagagaaaagcctgttt 180
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Db    251 accacaggggacaagattcttgatactgcactctctaagattggagagaaaagcctgttt 310

Qy    181 accaaggagcttgaacatgccctggagaagaatgaagtggacctggttgttcactccttg 240
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Db    311 accaaggagcttgaacatgccctggagaagaatgaagtggacctggttgttcactccttg 370

Qy    241 aaggacctgcccactgtgcttcctcctggcttcaccatcggagccatctgcaagcgggaa 300
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Db    371 aaggacctgcccactgtgcttcctcctggcttcaccatcggagccatctgcaagcgggaa 430

Qy    301 aaccctcatgatgctgttgtctttcacccaaaatttgttgggaagaccctagaaaccctg 360
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Db    431 aaccctcatgatgctgttgtctttcacccaaaatttgttgggaagaccctagaaaccctg 490

Qy    361 ccagagaagagtgtggtgggaaccagctccctgcgaagagcagcccagctgcagagaaag 420
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Db    491 ccagagaagagtgtggtgggaaccagctccctgcgaagagcagcccagctgcagagaaag 550

Qy    421 ttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttcggaagctg 480
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Db    551 ttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttcggaagctg 610

Qy    481 gacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatgggc 540
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Qy    541 tggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctgtgggccag 600
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Db    671 tggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctgtgggccag 730

Qy    601 ggggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtg 660
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Db    731 ggggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtg 790

Qy    661 ctgcacgatcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctg 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    791 ctgcacgatcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctg 850

Qy    721 gaaggaggctgcagtgtgccagtagccgtgcatacagctatgaaggatgggcaactgtac 780
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Db    851 gaaggaggctgcagtgtgccagtagccgtgcatacagctatgaaggatgggcaactgtac 910

Qy    781 ctgactggaggagtctggagtctagacggctcagatagcatacaagagaccatgcaggct 840
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Db    911 ctgactggaggagtctggagtctagacggctcagatagcatacaagagaccatgcaggct 970

Qy    841 accatccatgtccctgcccagcatgaagatggccctgaggatgacccacagttggtaggc 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    971 accatccatgtccctgcccagcatgaagatggccctgaggatgacccacagttggtaggc 1030

Qy    901 atcactgctcgtaacattccacgagggccccagttggctgcccagaacttgggcatcagc 960
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Qy    961 ctggccaacttgttgctgagcaaaggagccaaaaacatcctggatgttgcacggcaattg 1020
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Qy   1021 aacgatgcccattaa 1035
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Db   1151 aacgatgcccattaa 1165
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RESULT 6
AAX87639/c

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ID   AAX87639 standard; cDNA; 3988 BP.
XX
AC   AAX87639;
XX
DT   26-OCT-1999  (first entry)
XX
DE   Human porphobilinogen deaminase clone 1.1 in pBluescript SK-.
XX
KW   Porphobilinogen deaminase; human; haem; ALA deficiency porphyria;
KW   porphyria cutanea tarda; hereditary coproporphyria;
KW   harderoporphyria; congenital erythropoietic porphyria;
KW   variegata porphyria; erythropoietic protoporphyria;
KW   hepatoerythropoietic porphyria; acute intermittent porphyria;
KW   gene therapy; enzyme replacement therapy; plasmid pBluescript SK-;
KW   ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             complement (1730..696)
FT                   /*tag= a
XX
PN   WO9937325-A2.
XX
PD   29-JUL-1999.
XX
PF   27-JAN-1999;    99WO-DK00040.
XX
PR   30-DEC-1998;    98DK-0001748.
PR   27-JAN-1998;    98DK-0000112.
XX
PA   (HEME-) HEMEBIOTECH AS.
XX
PI   Fogh J,  Gellerfors P;
XX
DR   WPI; 1999-478987/40.
DR   P-PSDB; AAY06611.
XX
PT   Treatment of acute intermittent porphyria and other porphyric
PT   diseases using an enzyme belonging to the haem biosynthetic pathway
XX
PS   Disclosure; Fig 9a-x; 100pp; English.
XX
CC   This is the nucleotide sequence of human PBGD clone 1.1 (see
CC   AAX87630) in plasmid Bluescript SK-, allowing recombinant expression
CC   of porphobilinogen deaminase (PGGD, see AAY06611).  PBGD catalyses
CC   the rate-limiting step of the haem biosynthetic pathway.  Mutation
CC   of the PBGD gene is associated with the autosomal dominant disorder
CC   acute intermittent porphyria (AIP).  A claimed method of treating a
CC   patient having a mutation in the PBGD gene comprises using a human
CC   PBGD cDNA sequence of either non-erythropoietic form (see AAX87631)
CC   or erythopoietic form (especially clone 1.1 cDNA), according to the
CC   tissue in which PBGD should be expressed, and transfection of the
CC   patient with the relevant cDNA.  Gene therapy treatment of patients
CC   with AIP by a correction of one of the specific point mutations
CC   identified as causing the disease by use of chimeraplasty gene
CC   repair is also claimed.
XX
SQ   Sequence 3988 BP; 918 A; 1056 C; 1000 G; 1014 T; 0 other;
```

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  Query Match           100.0%;  Score 1035;  DB 20;  Length 3988;
  Best Local Similarity  100.0%;  Pred. No. 3.7e-279;
  Matches 1035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy      61 gtggtggcaacattgaaagcctcgtaccctggcctgcagtttgaaatcattgctatgtcc 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1670 GTGGTGGCAACATTGAAAGCCTCGTACCCTGGCCTGCAGTTTGAAATCATTGCTATGTCC 1611
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Qy     121 accacaggggacaagattcttgatactgcactctctaagattggagagaaaagcctgttt 180
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Db    1610 ACCACAGGGGACAAGATTCTTGATACTGCACTCTCTAAGATTGGAGAGAAAAGCCTGTTT 1551

Qy     181 accaaggagcttgaacatgccctggagaagaatgaagtggacctggttgttcactccttg 240
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Db    1550 ACCAAGGAGCTTGAACATGCCCTGGAGAAGAATGAAGTGGACCTGGTTGTTCACTCCTTG 1491

Qy     241 aaggacctgcccactgtgcttcctcctggcttcaccatcggagccatctgcaagcgggaa 300
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Db    1490 AAGGACCTGCCCACTGTGCTTCCTCCTGGCTTCACCATCGGAGCCATCTGCAAGCGGGAA 1431

Qy     301 aaccctcatgatgctgttgtctttcacccaaaatttgttgggaagaccctagaaaccctg 360
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Qy     361 ccagagaagagtgtggtgggaaccagctccctgcgaagagcagcccagctgcagagaaag 420
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Db    1310 TTCCCGCATCTGGAGTTCAGGAGTATTCGGGGAAACCTCAACACCCGGCTTCGGAAGCTG 1251

Qy     481 gacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatgggc 540
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Qy     541 tggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctgtgggccag 600
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Qy     601 ggggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtg 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1070 CTGCACGATCCCGAGACTCTGCTTCGCTGCATCGCTGAAAGGGCCTTCCTGAGGCACCTG 1011

Qy     721 gaaggaggctgcagtgtgccagtagccgtgcatacagctatgaaggatgggcaactgtac 780
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Qy     781 ctgactggaggagtctggagtctagacggctcagatagcatacaagagaccatgcaggct 840
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Qy     961 ctggccaacttgttgctgagcaaaggagccaaaaacatcctggatgttgcacggcaattg 1020
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Db     770 CTGGCCAACTTGTTGCTGAGCAAAGGAGCCAAAAACATCCTGGATGTTGCACGGCAATTG 711

Qy    1021 aacgatgcccattaa 1035
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RESULT 7
AAF72857/c
ID AAF72857 standard; DNA; 3988 BP.
XX
AC AAF72857;
XX
DT 24-APR-2001 (first entry)
XX
DE PDGB DNA.
XX
KW Heme biosynthetic pathway; gene therapy; AIP; ALA;
KW delta-aminolevulinic acid; deficient porphyria; ADP;
KW porphyria cutanea tarda; PCT; hereditary coproporphyria; HCP;
KW harderoporphyria; HDP; variegata porphyria; VP;
KW congenital erythropoietic porphyria; CEP;
KW erythropoietic protoporphyria; EPP;
KW hepatoerythropoietic porphyria; HEP; ds.
XX
OS Homo sapiens.
XX
PN WO200107065-A2.
XX
PD 01-FEB-2001.
XX
PF 27-JUL-2000; 2000WO-DK00425.
XX
PR 27-JUL-1999; 99DK-0001071.
PR 19-APR-2000; 2000DK-0000667.
XX
PA (HEME-) HEMEBIOTECH AS.
XX
PI Gellerfors P, Fogh J;
XX
DR WPI; 2001-159639/16.
XX
PT Treatment or prevention of porphyria, by enzyme replacement or gene
PT therapy for correction of mutations, particularly in the
PT porphorbilinogen deaminase gene -
XX
PS Disclosure; Page 203-205; 207pp; English.
XX
CC The present invention relates to treatment or prevention of a
CC disease caused by deficiency of at least one enzyme of the
CC heme biosynthetic pathway by administering at least one catalyst,
CC optionally combined with gene therapy of the relevant mutation.
CC The invention is useful for treating and/or preventing AIP, ALA
CC (delta-aminolevulinic acid) deficient porphyria (ADP), porphyria
CC cutanea tarda (PCT), hereditary coproporphyria (HCP), harderoporphyria
CC (HDP), variegata porphyria (VP), congenital erythropoietic porphyria
CC (CEP), erythropoietic protoporphyria (EPP) and hepatoerythropoietic
CC porphyria (HEP).
XX
SQ Sequence 3988 BP; 918 A; 1056 C; 1000 G; 1014 T; 0 other;

Query Match 100.0%; Score 1035; DB 22; Length 3988;
Best Local Similarity 100.0%; Pred. No. 3.7e-279;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     361 ccagagaagagtgtggtgggaaccagctccctgcgaagagcagcccagctgcagagaaag 420
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Qy    1021 aacgatgcccattaa 1035
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Db     710 AACGATGCCCATTAA 696


RESULT   8
AAX87632
ID   AAX87632 standard; cDNA; 1035 BP.
XX
AC   AAX87632;
XX
DT   26-OCT-1999  (first entry)
XX
DE   Human porphobilinogen deaminase clone 1.3.
XX
KW   Porphobilinogen deaminase; human; haem; ALA deficiency porphyria;
KW   porphyria cutanea tarda; hereditary coproporphyria;
KW   harderoporphyria; congenital erythropoietic porphyria;
KW   variegata porphyria; erythropoietic protoporphyria;
KW   hepatoerythropoietic porphyria; acute intermittent porphyria;
KW   gene therapy; enzyme replacement therapy; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(513,A)
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FT                   /note= "silent mutation"
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FT                   /note= "Asn to Thr substitution"
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PN   WO9937325-A2.
XX
PD   29-JUL-1999.
XX
PF   27-JAN-1999;   99WO-DK00040.
XX
PR   30-DEC-1998;   98DK-0001748.
PR   27-JAN-1998;   98DK-0000112.
XX
PA   (HEME-) HEMEBIOTECH AS.
XX
PI   Fogh J,  Gellerfors P;
XX
DR   WPI; 1999-478987/40.
XX
PT   Treatment of acute intermittent porphyria and other porphyric
PT   diseases using an enzyme belonging to the haem biosynthetic pathway
XX
PS   Disclosure; Page 92; 100pp; English.
XX
CC   This is the nucleotide sequence of human PBGD clone 1.3 coding for
CC   an erythropoietic expressed form of porphobilinogen deaminase (PBGD).
CC   This enzyme catalyses the third, rate-limiting step of the haem
CC   biosynthetic pathway.  PBGD was cloned from spleen, bone marrow,
CC   lymph node, lung, whole brain and adipose tissue cDNA using a
CC   nested PCR strategy.  8 PBGD clones were sequenced (see AAX87630 and
CC   AAX87632-38).  Clone 1.3, from spleen cDNA, has 6 changes from the
CC   previously published sequence.  Clone 1.1 (see AAX87630) represents
CC   the most prevalent 'wild-type' allele in the population.  Mutation
CC   of the PBGD gene is associated with the autosomal dominant disorder
CC   acute intermittent porphyria (AIP).  A claimed method of treating a
CC   patient having a mutation in the PBGD gene comprises using a human
CC   PBGD cDNA sequence of either non-erythropoietic form (see AAX87631)
CC   or erythopoietic form (especially clone 1.1 cDNA), according
CC   to the tissue in which PBGD should be expressed, and transfection
CC   of the patient with the relevant cDNA.  Gene therapy treatment of
CC   patients with AIP by a correction of one of the specific point
CC   mutations identified as causing the disease by use of chimeraplasty
CC   gene repair is also claimed.  Other enzymes involved in the haem
CC   biosynthetic pathway can also be used to treat various porphyrias.
XX
SQ   Sequence 1035 BP; 250 A; 271 C; 303 G; 211 T; 0 other;


  Query Match             99.8%;  Score 1033.4;  DB 20;  Length 1035;
  Best Local Similarity   99.9%;  Pred. No. 5.7e-279;
  Matches 1034;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy      61 gtggtggcaacattgaaagcctcgtaccctggcctgcagtttgaaatcattgctatgtcc 120
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Qy    301 aaccctcatgatgctgttgtctttcacccaaaatttgttgggaagaccctagaaaccctg 360
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Qy    361 ccagagaagagtgtggtgggaaccagctccctgcgaagagcagcccagctgcagagaaag 420
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Db    361 ccagagaagagtgtggtgggaaccagctccctgcgaagagcagcccagctgcagagaaag 420

Qy    421 ttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttcggaagctg 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttcggaagctg 480

Qy    481 gacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatgggc 540
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Qy    541 tggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctgtgggccag 600
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RESULT   9
AAX87633
ID   AAX87633 standard; cDNA; 1035 BP.
XX
AC   AAX87633;
XX
DT   26-OCT-1999  (first entry)
XX
DE   Human porphobilinogen deaminase clone 2.1.
XX
KW   Porphobilinogen deaminase; human; haem; ALA deficiency porphyria;
KW   porphyria cutanea tarda; hereditary coproporphyria;
KW   harderoporphyria; congenital erythropoietic porphyria;
KW   variegata porphyria; erythropoietic protoporphyria;
KW   hepatoerythropoietic porphyria; acute intermittent porphyria;
KW   gene therapy; enzyme replacement therapy; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(513,A)
FT                   /*tag= a
FT                   /note= "silent mutation"
FT   variation       replace(555,A)
FT                   /*tag= b
FT                   /note= "silent mutation"
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XX
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XX
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PR   27-JAN-1998;   98DK-0000112.
XX
PA   (HEME-) HEMEBIOTECH AS.
XX
PI   Fogh J,  Gellerfors P;
XX
DR   WPI; 1999-478987/40.
XX
PT   Treatment of acute intermittent porphyria and other porphyric
PT   diseases using an enzyme belonging to the haem biosynthetic pathway
XX
PS   Disclosure; Page 92-93; 100pp; English.
XX
CC   This is the nucleotide sequence of human PBGD clone 2.1 coding for
CC   an erythropoietic expressed form of porphobilinogen deaminase (PBGD).
CC   This enzyme catalyses the third, rate-limiting step of the haem
CC   biosynthetic pathway.  PBGD was cloned from spleen, bone marrow,
CC   lymph node, lung, whole brain and adipose tissue cDNA using a
CC   nested PCR strategy.  8 PBGD clones were sequenced (see AAX87630 and
CC   AAX87632-38). Clone 2.1, from bone marrow cDNA, has 6 changes from the
CC   previously published sequence.  Clone 1.1 (see AAX87630) represents
CC   the most prevalent 'wild-type' allele in the population.  Mutation
CC   of the PBGD gene is associated with the autosomal dominant disorder
CC   acute intermittent porphyria (AIP).  A claimed method of treating a
CC   patient having a mutation in the PBGD gene comprises using a human
CC   PBGD cDNA sequence of either non-erythropoietic form (see AAX87631)
CC   or erythopoietic form (especially clone 1.1 cDNA), according
CC   to the tissue in which PBGD should be expressed, and transfection
CC   of the patient with the relevant cDNA.  Gene therapy treatment of
CC   patients with AIP by a correction of one of the specific point
CC   mutations identified as causing the disease by use of chimeraplasty
CC   gene repair is also claimed.  Other enzymes involved in the haem
CC   biosynthetic pathway can also be used to treat various porphyrias.
XX
SQ   Sequence 1035 BP; 250 A; 271 C; 303 G; 211 T; 0 other;
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  Best Local Similarity   99.9%;  Pred. No. 5.7e-279;
  Matches 1034;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy     181 accaaggagcttgaacatgccctggagaagaatgaagtggacctggttgttcactccttg 240
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Db     181 accaaggagcttgaacatgccctggagaagaatgaagtggacctggttgttcactccttg 240

Qy     241 aaggacctgcccactgtgcttcctcctggcttcaccatcggagccatctgcaagcgggaa 300
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Db     241 aaggacctgcccactgtgcttcctcctggcttcaccatcggagccatctgcaagcgggaa 300

Qy     301 aaccctcatgatgctgttgtctttcacccaaaatttgttgggaagaccctagaaaccctg 360
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Qy     361 ccagagaagagtgtggtgggaaccagctccctgcgaagagcagcccagctgcagagaaag 420
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Db     361 ccagagaagagtgtggtgggaaccagctccctgcgaagagcagcccagctgcagagaaag 420

Qy     421 ttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttcggaagctg 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 ttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttcggaagctg 480

Qy     481 gacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatgggc 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 gacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatgggc 540

Qy     541 tggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctgtgggccag 600
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Qy     601 ggggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtg 660
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Qy     661 ctgcacgatcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctg 720
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Qy     721 gaaggaggctgcagtgtgccagtagccgtgcatacagctatgaaggatgggcaactgtac 780
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Qy     781 ctgactggaggagtctggagtctagacggctcagatagcatacaagagaccatgcaggct 840
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Qy     841 accatccatgtccctgcccagcatgaagatggccctgaggatgacccacagttggtaggc 900
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Qy     961 ctggccaacttgttgctgagcaaaggagccaaaaacatcctggatgttgcacggcaattg 1020
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Qy    1021 aacgatgcccattaa 1035
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RESULT  10
AAF72850
ID   AAF72850 standard; DNA; 1035 BP.
XX
AC   AAF72850;
XX
DT   24-APR-2001  (first entry)
XX
DE   PDGB from spleen.
XX
KW   Heme biosynthetic pathway; gene therapy; AIP; ALA;
KW   delta-aminolevulinic acid; deficient porphyria; ADP;
KW   porphyria cutanea tarda; PCT; hereditary coproporphyria; HCP;
KW   harderoporphyria; HDP; variegata porphyria; VP;
KW   congenital erythropoietic porphyria; CEP;
KW   erythropoietic protoporphyria; EPP;
KW   hepatoerythropoietic porphyria; HEP; ds.
XX
OS   Homo sapiens.
XX
PN   WO200107065-A2.
XX
PD   01-FEB-2001.
XX
PF   27-JUL-2000; 2000WO-DK00425.
XX
PR   27-JUL-1999;   99DK-0001071.
PR   19-APR-2000; 2000DK-0000667.
XX
PA   (HEME-) HEMEBIOTECH AS.
XX
PI   Gellerfors P,  Fogh J;
XX
DR   WPI; 2001-159639/16.
XX
PT   Treatment or prevention of porphyria, by enzyme replacement or gene
PT   therapy for correction of mutations, particularly in the
PT   porphorbilinogen deaminase gene  -
XX
PS   Disclosure; Page 200-201; 207pp; English.
XX
CC   The present invention relates to treatment or prevention of a
CC   disease caused by deficiency of at least one enzyme of the
CC   heme biosynthetic pathway by administering at least one catalyst,
CC   optionally combined with gene therapy of the relevant mutation.
CC   The invention is useful for treating and/or preventing AIP, ALA
CC   (delta-aminolevulinic acid) deficient porphyria (ADP), porphyria
CC   cutanea tarda (PCT), hereditary coproporphyria (HCP), harderoporphyria
CC   (HDP), variegata porphyria (VP), congenital erythropoietic porphyria
CC   (CEP ), erythropoietic protoporphyria (EPP) and hepatoerythropoietic
CC   porphyria (HEP).
XX
SQ   Sequence 1035 BP; 250 A; 271 C; 303 G; 211 T; 0 other;
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  Query Match             99.8%;  Score 1033.4;  DB 22;  Length 1035;
  Best Local Similarity   99.9%;  Pred. No. 5.7e-279;
  Matches 1034;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db       1 atgagagtgattcgcgtgggtacccgcaagagccagcttgctcgcatacagacggacagt 60

Qy      61 gtggtggcaacattgaaagcctcgtaccctggcctgcagtttgaaatcattgctatgtcc 120
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Db      61 gtggtggcaacattgaaagcctcgtaccctggcctgcagtttgaaatcattgctatgtcc 120
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Qy    121 accacaggggacaagattcttgatactgcactctctaagattggagagaaaagcctgttt 180
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Db    121 accacaggggacaagattcttgatactgcactctctaagattggagagaaaagcctgttt 180

Qy    181 accaaggagcttgaacatgccctggagaagaatgaagtggacctggttgttcactccttg 240
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Qy    241 aaggacctgcccactgtgcttcctcctggcttcaccatcggagccatctgcaagcgggaa 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 aaggacctgcccactgtgcttcctcctggcttcaccatcggagccatctgcaagcgggaa 300

Qy    301 aaccctcatgatgctgttgtctttcacccaaaatttgttgggaagaccctagaaaccctg 360
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Db    301 aaccctcatgatgctgttgtctttcacccaaaatttgttgggaagaccctagaaaccctg 360

Qy    361 ccagagaagagtgtggtgggaaccagctccctgcgaagagcagcccagctgcagagaaag 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ccagagaagagtgtggtgggaaccagctccctgcgaagagcagcccagctgcagagaaag 420

Qy    421 ttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttcggaagctg 480
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Db    421 ttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttcggaagctg 480

Qy    481 gacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatgggc 540
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Db    481 gacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatgggc 540

Qy    541 tggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctgtgggccag 600
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    541 tggcacaaccgggtggggcagatcctgcaccctgaggaatgcatgtatgctgtgggccag 600

Qy    601 ggggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtg 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 ggggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtg 660

Qy    661 ctgcacgatcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctg 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ctgcacgatcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctg 720

Qy    721 gaaggaggctgcagtgtgccagtagccgtgcatacagctatgaaggatgggcaactgtac 780
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Db    721 gaaggaggctgcagtgtgccagtagccgtgcatacagctatgaaggatgggcaactgtac 780

Qy    781 ctgactggaggagtctggagtctagacggctcagatagcatacaagagaccatgcaggct 840
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Db    781 ctgactggaggagtctggagtctagacggctcagatagcatacaagagaccatgcaggct 840

Qy    841 accatccatgtccctgcccagcatgaagatggccctgaggatgacccacagttggtaggc 900
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Db    841 accatccatgtccctgcccagcatgaagatggccctgaggatgacccacagttggtaggc 900

Qy    901 atcactgctcgtaacattccacgagggccccagttggctgcccagaacttgggcatcagc 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 atcactgctcgtaacattccacgagggccccagttggctgcccagaacttgggcatcagc 960

Qy    961 ctggccaacttgttgctgagcaaaggagccaaaaacatcctggatgttgcacggcaattg 1020
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Db    961 ctggccaacttgttgctgagcaaaggagccaaaaacatcctggatgttgcacggcaattg 1020

Qy   1021 aacgatgcccattaa 1035
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RESULT  11
AAF72851
ID   AAF72851 standard; DNA; 1035 BP.
XX
AC   AAF72851;
XX
DT   24-APR-2001  (first entry)
XX
DE   PDGB from bone marrow #1.
XX
KW   Heme biosynthetic pathway; gene therapy; AIP; ALA;
KW   delta-aminolevulinic acid; deficient porphyria; ADP;
KW   porphyria cutanea tarda; PCT; hereditary coproporphyria; HCP;
KW   harderoporphyria; HDP; variegata porphyria; VP;
KW   congenital erythropoietic porphyria; CEP;
KW   erythropoietic protoporphyria; EPP;
KW   hepatoerythropoietic porphyria; HEP; ds.
XX
OS   Homo sapiens.
XX
PN   WO200107065-A2.
XX
PD   01-FEB-2001.
XX
PF   27-JUL-2000; 2000WO-DK00425.
XX
PR   27-JUL-1999;   99DK-0001071.
PR   19-APR-2000; 2000DK-0000667.
XX
PA   (HEME-) HEMEBIOTECH AS.
XX
PI   Gellerfors P,  Fogh J;
XX
DR   WPI; 2001-159639/16.
XX
PT   Treatment or prevention of porphyria, by enzyme replacement or gene
PT   therapy for correction of mutations, particularly in the
PT   porphorbilinogen deaminase gene  -
XX
PS   Disclosure; Page 201; 207pp; English.
XX
CC   The present invention relates to treatment or prevention of a
CC   disease caused by deficiency of at least one enzyme of the
CC   heme biosynthetic pathway by administering at least one catalyst,
CC   optionally combined with gene therapy of the relevant mutation.
CC   The invention is useful for treating and/or preventing AIP, ALA
CC   (delta-aminolevulinic acid) deficient porphyria (ADP), porphyria
CC   cutanea tarda (PCT), hereditary coproporphyria (HCP), harderoporphyria
CC   (HDP), variegata porphyria (VP), congenital erythropoietic porphyria
CC   (CEP ), erythropoietic protoporphyria (EPP) and hepatoerythropoietic
CC   porphyria (HEP).
XX
SQ   Sequence 1035 BP; 250 A; 271 C; 303 G; 211 T; 0 other;
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  Query Match           99.8%;  Score 1033.4;  DB 22;  Length 1035;
  Best Local Similarity   99.9%;  Pred. No. 5.7e-279;
  Matches 1034;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy    121 accacaggggacaagattcttgatactgcactctctaagattggagagaaaagcctgttt 180
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Qy    301 aaccctcatgatgctgttgtctttcacccaaaatttgttgggaagaccctagaaaccctg 360
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Qy     601 ggggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtg 660
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Qy     661 ctgcacgatcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctg 720
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Db     661 ctgcacgatcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctg 720

Qy     721 gaaggaggctgcagtgtgccagtagccgtgcatacagctatgaaggatgggcaactgtac 780
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Qy     961 ctggccaacttgttgctgagcaaaggagccaaaaacatcctggatgttgcacggcaattg 1020
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Qy    1021 aacgatgcccattaa 1035
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Db    1021 aacgatgcccattaa 1035


RESULT 12
AAX87636
ID   AAX87636 standard; cDNA; 1035 BP.
XX
AC   AAX87636;
XX
DT   26-OCT-1999  (first entry)
XX
DE   Human porphobilinogen deaminase clone 3.3.
XX
KW   Porphobilinogen deaminase; human; haem; ALA deficiency porphyria;
KW   porphyria cutanea tarda; hereditary coproporphyria;
KW   harderoporphyria; congenital erythropoietic porphyria;
KW   variegata porphyria; erythropoietic protoporphyria;
KW   hepatoerythropoietic porphyria; acute intermittent porphyria;
KW   gene therapy; enzyme replacement therapy; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /note= "silent mutation"
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FT   variation       replace(729,C)
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FT                   /*tag= d
FT                   /note= "Asn to Thr substitution"
FT   variation       replace(1017,G)
FT                   /*tag= e
FT                   /note= "silent mutation"
FT   variation       replace(1018,C)
FT                   /*tag= f
FT                   /note= "silent mutation"
FT   variation       replace(1020,T)
FT                   /*tag= g
FT                   /note= "silent mutation"
XX
PN   WO9937325-A2.
XX
PD   29-JUL-1999.
XX
PF   27-JAN-1999;   99WO-DK00040.
XX
PR   30-DEC-1998;   98DK-0001748.
PR   27-JAN-1998;   98DK-0000112.
XX
PA   (HEME-) HEMEBIOTECH AS.
XX
PI   Fogh J,  Gellerfors P;
XX
DR   WPI; 1999-478987/40.
XX
PT   Treatment of acute intermittent porphyria and other porphyric
PT   diseases using an enzyme belonging to the haem biosynthetic pathway
XX
PS   Disclosure; Page 94; 100pp; English.
XX
CC   This is the nucleotide sequence of human PBGD clone 3.3 coding for
CC   an erythropoietic expressed form of porphobilinogen deaminase (PBGD).
CC   This enzyme catalyses the third, rate-limiting step of the haem
CC   biosynthetic pathway.  PBGD was cloned from spleen, bone marrow,
CC   lymph node, lung, whole brain and adipose tissue cDNA using a
CC   nested PCR strategy.  8 PBGD clones were sequenced (see AAX87630 and
CC   AAX87632-38). Clone 3.3, from lymph node cDNA, has 6 changes from the
CC   previously published sequence.  Clone 1.1 (see AAX87630) represents
CC   the most prevalent 'wild-type' allele in the population.  Mutation
CC   of the PBGD gene is associated with the autosomal dominant disorder
CC   acute intermittent porphyria (AIP).  A claimed method of treating a
CC   patient having a mutation in the PBGD gene comprises using a human
CC   PBGD cDNA sequence of either non-erythropoietic form (see AAX87631)
CC   or erythopoietic form (especially clone 1.1 cDNA), according
CC   to the tissue in which PBGD should be expressed, and transfection
CC   of the patient with the relevant cDNA.  Gene therapy treatment of
CC   patients with AIP by a correction of one of the specific point
CC   mutations identified as causing the disease by use of chimeraplasty
CC   gene repair is also claimed.  Other enzymes involved in the haem
CC   biosynthetic pathway can also be used to treat various porphyrias.
XX
SQ   Sequence 1035 BP; 250 A; 270 C; 303 G; 212 T; 0 other;


  Query Match             99.7%;  Score 1031.8;  DB 20;  Length 1035;
  Best Local Similarity   99.8%;  Pred. No. 1.6e-278;
  Matches 1033;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Qy      61 gtggtggcaacattgaaagcctcgtaccctggcctgcagtttgaaatcattgctatgtcc 120
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Db     61 gtggtggcaacattgaaagcctcgtaccctggcctgcagtttgaaatcattgctatgtcc 120

Qy    121 accacaggggacaagattcttgatactgcactctctaagattggagagaaaagcctgttt 180
Db    121 accacaggggacaagattcttgatactgcactctctaagattggagagaaaagcctgttt 180

Qy    181 accaaggagcttgaacatgccctggagaagaatgaagtggacctggttgttcactccttg 240
Db    181 accaaggagcttgaacatgccctggagaagaatgaagtggacctggttgttcactccttg 240

Qy    241 aaggacctgcccactgtgcttcctcctggcttcaccatcggagccatctgcaagcgggaa 300
Db    241 aaggacctgcccactgtgcttcctcctggcttcaccatcggagccatctgcaagcgggaa 300

Qy    301 aaccctcatgatgctgttgtctttcacccaaaatttgttgggaagaccctagaaaccctg 360
Db    301 aaccctcatgatgctgttgtctttcacccaaaatttgttgggaagaccctagaaaccctg 360

Qy    361 ccagagaagagtgtggtgggaaccagctccctgcgaagagcagcccagctgcagagaaag 420
Db    361 ccagagaagagtgtggtgggaaccagctccctgcgaagagcagcccagctgcagagaaag 420

Qy    421 ttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttcggaagctg 480
Db    421 ttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttcggaagctg 480

Qy    481 gacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatgggc 540
Db    481 gacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatgggc 540

Qy    541 tggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctgtgggccag 600
Db    541 tggcacaaccgggtggggcagatcctgcaccctgaggaatgcatgtatgctgtgggccag 600

Qy    601 ggggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtg 660
Db    601 ggggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtg 660

Qy    661 ctgcacgatcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctg 720
Db    661 ctgcacgatcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctg 720

Qy    721 gaaggaggctgcagtgtgccagtagccgtgcatacagctatgaaggatgggcaactgtac 780
Db    721 gaaggaggttgcagtgtgccagtagccgtgcatacagctatgaaggatgggcaactgtac 780

Qy    781 ctgactggaggagtctggagtctagacggctcagatagcatacaagagaccatgcaggct 840
Db    781 ctgactggaggagtctggagtctagacggctcagatagcatacaagagaccatgcaggct 840

Qy    841 accatccatgtccctgcccagcatgaagatggccctgaggatgacccacagttggtaggc 900
Db    841 accatccatgtccctgcccagcatgaagatggccctgaggatgacccacagttggtaggc 900

Qy    901 atcactgctcgtaacattccacgagggccccagttggctgcccagaacttgggcatcagc 960
Db    901 atcactgctcgtaacattccacgagggccccagttggctgcccagaacttgggcatcagc 960

Qy    961 ctggccaacttgttgctgagcaaaggagccaaaaacatcctggatgttgcacggcaattg 1020
Db    961 ctggccaacttgttgctgagcaaaggagccaaaaacatcctggatgttgcacggcaattg 1020

Qy   1021 aacgatgcccattaa 1035
Db   1021 aacgatgcccattaa 1035
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RESULT 13
AAF72854
ID   AAF72854 standard; DNA; 1035 BP.
XX
AC   AAF72854;
XX
DT   24-APR-2001  (first entry)
XX
DE   PDGB from lymph node #2.
XX
KW   Heme biosynthetic pathway; gene therapy; AIP; ALA;
KW   delta-aminolevulinic acid; deficient porphyria; ADP;
KW   porphyria cutanea tarda; PCT; hereditary coproporphyria; HCP;
KW   harderoporphyria; HDP; variegata porphyria; VP;
KW   congenital erythropoietic porphyria; CEP;
KW   erythropoietic protoporphyria; EPP;
KW   hepatoerythropoietic porphyria; HEP; ds.
XX
OS   Homo sapiens.
XX
PN   WO200107065-A2.
XX
PD   01-FEB-2001.
XX
PF   27-JUL-2000; 2000WO-DK00425.
XX
PR   27-JUL-1999;   99DK-0001071.
PR   19-APR-2000; 2000DK-0000667.
XX
PA   (HEME-) HEMEBIOTECH AS.
XX
PI   Gellerfors P,  Fogh J;
XX
DR   WPI; 2001-159639/16.
XX
PT   Treatment or prevention of porphyria, by enzyme replacement or gene
PT   therapy for correction of mutations, particularly in the
PT   porphorbilinogen deaminase gene  -
XX
PS   Disclosure; Page 202; 207pp; English.
XX
CC   The present invention relates to treatment or prevention of a
CC   disease caused by deficiency of at least one enzyme of the
CC   heme biosynthetic pathway by administering at least one catalyst,
CC   optionally combined with gene therapy of the relevant mutation.
CC   The invention is useful for treating and/or preventing AIP, ALA
CC   (delta-aminolevulinic acid) deficient porphyria (ADP), porphyria
CC   cutanea tarda (PCT), hereditary coproporphyria (HCP), harderoporphyria
CC   (HDP), variegata porphyria (VP), congenital erythropoietic porphyria
CC   (CEP ), erythropoietic protoporphyria (EPP) and hepatoerythropoietic
CC   porphyria (HEP).
XX
SQ   Sequence 1035 BP; 250 A; 270 C; 303 G; 212 T; 0 other;
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  Matches 1033;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Qy    241 aaggacctgcccactgtgcttcctcctggcttcaccatcggagccatctgcaagcgggaa 300
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Qy     361 ccagagaagagtgtggtgggaaccagctccctgcgaagagcagcccagctgcagagaaag 420
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Qy     421 ttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttcggaagctg 480
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Qy     481 gacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatgggc 540
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Qy     661 ctgcacgatcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctg 720
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RESULT 14
AAX87638
ID   AAX87638 standard; cDNA; 1035 BP.
XX
AC   AAX87638;
XX
DT   26-OCT-1999  (first entry)
XX
DE   Human porphobilinogen deaminase clone 6.1.
XX
KW   Porphobilinogen deaminase; human; haem; ALA deficiency porphyria;
KW   porphyria cutanea tarda; hereditary coproporphyria;
KW   harderoporphyria; congenital erythropoietic porphyria;
KW   variegata porphyria; erythropoietic protoporphyria;
KW   hepatoerythropoietic porphyria; acute intermittent porphyria;
KW   gene therapy; enzyme replacement therapy; ds.
XX
OS   Homo sapiens.
XX
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FT                   /note= "silent mutation"
FT   variation       replace(840,T)
FT                   /*tag= c
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FT                   /note= "Ala to Thr substitution"
FT   variation       replace(995,C)
FT                   /*tag= e
FT                   /note= "Asn to Thr substitution"
FT   variation       replace(1017,G)
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FT                   /note= "silent mutation"
FT   variation       replace(1018,C)
FT                   /*tag= g
FT                   /note= "silent mutation"
FT   variation       replace(1020)
FT                   /*tag= h
FT                   /note= "T deletion, frameshift"
XX
PN   WO9937325-A2.
XX
PD   29-JUL-1999.
XX
PF   27-JAN-1999;   99WO-DK00040.
XX
PR   30-DEC-1998;   98DK-0001748.
PR   27-JAN-1998;   98DK-0000112.
XX
PA   (HEME-) HEMEBIOTECH AS.
XX
PI   Fogh J,  Gellerfors P;
XX
DR   WPI; 1999-478987/40.
XX
PT   Treatment of acute intermittent porphyria and other porphyric
PT   diseases using an enzyme belonging to the haem biosynthetic pathway
XX
PS   Disclosure; Page 95; 100pp; English.
XX
CC   This is the nucleotide sequence of human PBGD clone 6.1 coding for
CC   an erythropoietic expressed form of porphobilinogen deaminase (PBGD).
CC   This enzyme catalyses the third, rate-limiting step of the haem
CC   biosynthetic pathway.  PBGD was cloned from spleen, bone marrow,
CC   lymph node, lung, whole brain and adipose tissue cDNA using a
CC   nested PCR strategy.  8 PBGD clones were sequenced (see AAX87630 and
CC   AAX87632-38). Clone 6.1, from whole brain cDNA, has 8 changes from the
CC   previously published sequence.  Clone 1.1 (see AAX87630) represents
CC   the most prevalent 'wild-type' allele in the population.  Mutation
CC   of the PBGD gene is associated with the autosomal dominant disorder
CC   acute intermittent porphyria (AIP).  A claimed method of treating a
CC   patient having a mutation in the PBGD gene comprises using a human
CC   PBGD cDNA sequence of either non-erythropoietic form (see AAX87631)
CC   or erythopoietic form (especially clone 1.1 cDNA), according
CC   to the tissue in which PBGD should be expressed, and transfection
CC   of the patient with the relevant cDNA.  Gene therapy treatment of
CC   patients with AIP by a correction of one of the specific point
CC   mutations identified as causing the disease by use of chimeraplasty
CC   gene repair is also claimed.  Other enzymes involved in the haem
CC   biosynthetic pathway can also be used to treat various porphyrias.
XX
SQ   Sequence 1035 BP; 251 A; 272 C; 302 G; 210 T; 0 other;
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Query Match             99.5%;  Score 1030.2;  DB 20;  Length 1035;
Best Local Similarity   99.7%;  Pred. No. 4.5e-278;
Matches 1032;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
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Qy    181 accaaggagcttgaacatgccctggagaagaatgaagtggacctggttgttcactccttg 240
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Qy    241 aaggacctgcccactgtgcttcctcctggcttcaccatcggagccatctgcaagcgggaa 300
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Qy    301 aaccctcatgatgctgttgtctttcacccaaaatttgttgggaagaccctagaaaccctg 360
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Db    301 aaccctcatgatgctgttgtctttcacccaaaatttgttgggaagaccctagaaaccctg 360

Qy    361 ccagagaagagtgtggtgggaaccagctccctgcgaagagcagcccagctgcagagaaag 420
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Db    361 ccagagaagagtgtggtgggaaccagctccctgcgaagagcagcccagctgcagagaaag 420

Qy    421 ttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttcggaagctg 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    481 gacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatgggc 540
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Db    481 gacgagcagcaggagttcagtgccatcatcctggcaacagctggcctgcagcgcatgggc 540

Qy    541 tggcacaaccgggttgggcagatcctgcaccctgaggaatgcatgtatgctgtgggccag 600
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    541 tggcacaaccgggtggggcagatcctgcaccctgaggaatgcatgtatgctgtgggccag 600

Qy    601 ggggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtg 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    781 ctgactggaggagtctggagtctagacggctcagatagcatacaagagaccatgcaggct 840
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Qy    841 accatccatgtccctgcccagcatgaagatggccctgaggatgacccacagttggtaggc 900
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Db    901 atcactgctcgtaacattccacgagggccccagttggctgcccagaacttgggcatcagc 960

Qy    961 ctggccaacttgttgctgagcaaaggagccaaaaacatcctggatgttgcacggcaattg 1020
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RESULT 15
AAF72856
ID   AAF72856 standard; DNA; 1035 BP.
XX
AC   AAF72856;
XX
DT   24-APR-2001  (first entry)
XX
DE   PDGB from total brain #2.
XX
KW   Heme biosynthetic pathway; gene therapy; AIP; ALA;
KW   delta-aminolevulinic acid; deficient porphyria; ADP;
KW   porphyria cutanea tarda; PCT; hereditary coproporphyria; HCP;
KW   harderoporphyria; HDP; variegata porphyria; VP;
KW   congenital erythropoietic porphyria; CEP;
KW   erythropoietic protoporphyria; EPP;
KW   hepatoerythropoietic porphyria; HEP; ds.
XX
OS   Homo sapiens.
XX
PN   WO200107065-A2.
XX
PD   01-FEB-2001.
XX
PF   27-JUL-2000; 2000WO-DK00425.
XX
PR   27-JUL-1999;   99DK-0001071.
PR   19-APR-2000; 2000DK-0000667.
XX
PA   (HEME-) HEMEBIOTECH AS.
XX
PI   Gellerfors P,  Fogh J;
XX
DR   WPI; 2001-159639/16.
XX
PT   Treatment or prevention of porphyria, by enzyme replacement or gene
PT   therapy for correction of mutations, particularly in the
PT   porphorbilinogen deaminase gene  -
XX
PS   Disclosure; Page 203; 207pp; English.
XX
CC   The present invention relates to treatment or prevention of a
CC   disease caused by deficiency of at least one enzyme of the
CC   heme biosynthetic pathway by administering at least one catalyst,
CC   optionally combined with gene therapy of the relevant mutation.
CC   The invention is useful for treating and/or preventing AIP, ALA
CC   (delta-aminolevulinic acid) deficient porphyria (ADP), porphyria
CC   cutanea tarda (PCT), hereditary coproporphyria (HCP), harderoporphyria
CC   (HDP), variegata porphyria (VP), congenital erythropoietic porphyria
CC   (CEP ), erythropoietic protoporphyria (EPP) and hepatoerythropoietic
CC   porphyria (HEP).
XX
SQ   Sequence 1035 BP; 251 A; 272 C; 302 G; 210 T; 0 other;
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  Query Match            99.5%;  Score 1030.2;  DB 22;  Length 1035;
  Best Local Similarity  99.7%;  Pred. No. 4.5e-278;
  Matches 1032;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

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GenCore version 4.5

OM nucleic - nucleic search, using sw model

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Perfect score: 1113
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1103.4	99.1	1377	93	HSPBGDR2	X04808 Human mRNA
5	1046	94.0	1380	93	HSPBGDR	X04217 Human mRNA
6	1035	93.0	1035	9	AX020182	AX020182 Sequence
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	17	1032.6	92.8	5446	10	AX079025 AX079025 Sequence
	18	1031.8	92.7	1035	9	AX020187 AX020187 Sequence
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ALIGNMENTS

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VERSION     AX020193.1  GI:10043984
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1113)
  AUTHORS   Fogh,J. and Gellerfors,P.
  TITLE     Method for treating acute intermittent porphyria (aip) and other
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  JOURNAL   Patent: WO 9937325-A 12 29-JUL-1999;
            FOGH JENS (DK); HEMEBIOTECH A S (DK); GELLERFORS PAER (SE)
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VERSION     AX079028.1  GI:13158603
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SOURCE      human.
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REFERENCE   1  (bases 1 to 1113)
  AUTHORS   Gellerfors,P. and Fogh,J.
  TITLE     Production of rhpbgd and new therapeutic methods for treating
            patients with acute intermittent porphyria (aip) and other
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  JOURNAL   Patent: WO 0107065-A 4 01-FEB-2001;
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Qy     901 caagagaccatgcaggctaccatccatgtccctgcccagcatgaagatggccctgaggat 960
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Db     901 CAAGAGACCATGCAGGCTACCATCCATGTCCCTGCCCAGCATGAAGATGGCCCTGAGGAT 960

Qy     961 gacccacagttggtaggcatcactgctcgtaacattccacgagggccccagttggctgcc 1020
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Db     961 GACCCACAGTTGGTAGGCATCACTGCTCGTAACATTCCACGAGGGCCCCAGTTGGCTGCC 1020

Qy    1021 cagaacttgggcatcagcctggccaacttgttgctgagcaaaggagccaaaaacatcctg 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CAGAACTTGGGCATCAGCCTGGCCAACTTGTTGCTGAGCAAAGGAGCCAAAAACATCCTG 1080

Qy    1081 gatgttgcacggcaattgaacgatgcccattaa 1113
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Db    1081 GATGTTGCACGGCAATTGAACGATGCCCATTAA 1113
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RESULT   3
BC000520
LOCUS       BC000520      1545 bp    mRNA            PRI       16-MAR-2001
DEFINITION  Homo sapiens, hydroxymethylbilane synthase, clone MGC:8561, mRNA,
            complete cds.
ACCESSION   BC000520
VERSION     BC000520.1  GI:12653496
KEYWORDS    MGC.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1545)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-NOV-2000) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: DCTD/DTP
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site:       http://www.nisc.nih.gov/
            Contact:        nisc_mgc@nhgri.nih.gov
            Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
            Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
            Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
            McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
            Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
            Zhang,L.-H. and Green,E.D.
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            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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FEATURES             Location/Qualifiers
     source          1. .1545
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                     /clone="MGC:8561 IMAGE:2822949"
                     /tissue_type="Lung, small cell carcinoma"
                     /clone_lib="NIH_MGC_7"
                     /lab_host="DH10B-R"
                     /note="Vector: pOTB7"
     CDS             161. .1246
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                     /protein_id="AAH00520.1"
                     /db_xref="GI:12653497"
                     /translation="MSGNGNAAATAEENSPKMRVIRVGTRKSQLARIQTDSVVATLKA
                     SYPGLQFEIIAMSTTGDKILDTALSKIGEKSLFTKELEHALEKNEVDLVVHSLKDLPT
                     VLPPGFTIGAICKRENPHDAVVFHPKFVGKTLETLPEKSVVGTSSLRRAAQLQRKFPH
                     LEFRSIRGNLNTRLRKLDEQQEFSAIILATAGLQRMGWHNRVGQILHPEECMYAVGQG
                     ALGVEVRAKDQDILDLVGVLHDPETLLRCIAERAFLRHLEGGCSVPVAVHTAMKDGQL
                     YLTGGVWSLDGSDSIQETMQATIHVPAQHEDGPEDDPQLVGITARNIPRGPQLAAQNL
                     GISLANLLLSKGAKNILDVARQLNDAH"
BASE COUNT      380 a    413 c    443 g    309 t
ORIGIN
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  Best Local Similarity   99.6%;  Pred. No. 1.1e-254;
  Matches 1109;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 cacacagcctactttccaagcggagccatgtctggtaacggcaatgcggctgcaacggcg 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     134 CACACAGCCTACTTTCCAAGCGGAGCCATGTCTGGTAACGGCAATGCGGCTGCAACGGCG 193

Qy      61 gaagaaaacagcccaaagatgagagtgattcgcgtgggtacccgcaagagccagcttgct 120
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Db     194 GAAGAAAACAGCCCAAAGATGAGAGTGATTCGCGTGGGTACCCGCAAGAGCCAGCTTGCT 253

Qy     121 cgcatacagacggacagtgtggtggcaacattgaaagcctcgtaccctggcctgcagttt 180
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Db     254 CGCATACAGACGGACAGTGTGGTGGCAACATTGAAAGCCTCGTACCCTGGCCTGCAGTTT 313

Qy     181 gaaatcattgctatgtccaccacagggacaagattcttgatactgcactctctaagatt 240
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Db     314 GAAATCATTGCTATGTCCACCACAGGGACAAGATTCTTGATACTGCACTCTCTAAGATT 373

Qy     241 ggagagaaaagcctgtttaccaaggagcttgaacatgccctggagaagaatgaagtggac 300
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Db     374 GGAGAGAAAAGCCTGTTTACCAAGGAGCTTGAACATGCCCTGGAGAAGAATGAAGTGGAC 433

Qy     301 ctggttgttcactccttgaaggacctgcccactgtgcttcctcctggcttcaccatcgga 360
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Db     434 CTGGTTGTTCACTCCTTGAAGGACCTGCCCACTGTGCTTCCTCCTGGCTTCACCATCGGA 493

Qy     361 gccatctgcaagcgggaaaaccctcatgatgctgttgtctttcacccaaaatttgttggg 420
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Db     494 GCCATCTGCAAGCGGGAAAACCCTCATGATGCTGTTGTCTTTCACCCAAAATTTGTTGGG 553

Qy     421 aagaccctagaaaccctgccagagaagagtgtggtgggaaccagctccctgcgaagagca 480
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Db     554 AAGACCCTAGAAACCCTGCCAGAGAAGAGTGTGGTGGGAACCAGCTCCCTGCGAAGAGCA 613

Qy     481 gcccagctgcagagaaagttcccgcatctggagttcaggagtattcggggaaacctcaac 540
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Db     614 GCCCAGCTGCAGAGAAAGTTCCCGCATCTGGAGTTCAGGAGTATTCGGGGAAACCTCAAC 673

Qy     541 acccggcttcggaagctggacgagcagcaggagttcagtgccatcatcctggcaacagct 600
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Db     674 ACCCGGCTTCGGAAGCTGGACGAGCAGCAGGAGTTCAGTGCCATCATCCTGGCAACAGCT 733

Qy     601 ggcctgcagcgcatgggctggcacaaccgggttgggcagatcctgcaccctgaggaatgc 660
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Db     734 GGCCTGCAGCGCATGGGCTGGCACAACCGGGTGGGGCAGATCCTGCACCCTGAGGAATGC 793

Qy     661 atgtatgctgtgggccaggggggccttgggcgtggaagtgcgagccaaggaccaggacatc 720
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Db     794 ATGTATGCTGTGGGCCAGGGGGCCTTGGGCGTGGAAGTGCGAGCCAAGGACCAGGACATC 853

Qy     721 ttggatctggtgggtgtgctgcacgatcccgagactctgcttcgctgcatcgctgaaagg 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     854 TTGGATCTGGTGGGTGTGCTGCACGATCCCGAGACTCTGCTTCGCTGCATCGCTGAAAGG 913

Qy     781 gccttcctgaggcacctggaaggaggctgcagtgtgccagtagccgtgcatacagctatg 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     914 GCCTTCCTGAGGCACCTGGAAGGAGGCTGCAGTGTGCCAGTAGCCGTGCATACAGCTATG 973

Qy     841 aaggatgggcaactgtacctgactggaggagtctggagtctagacggctcagatagcata 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     974 AAGGATGGGCAACTGTACCTGACTGGAGGAGTCTGGAGTCTAGACGGCTCAGATAGCATA 1033

Qy     901 caagagaccatgcaggctaccatccatgtccctgcccagcatgaagatggccctgaggat 960
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Db    1034 CAAGAGACCATGCAGGCTACCATCCATGTCCCTGCCCAGCATGAAGATGGCCCTGAGGAT 1093

Qy     961 gacccacagttggtaggcatcactgctcgtaacattccacgagggccccagttggctgcc 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1094 GACCCACAGTTGGTAGGCATCACTGCTCGTAACATTCCACGAGGGCCCCAGTTGGCTGCC 1153

Qy    1021 cagaacttgggcatcagcctggccaacttgttgctgagcaaaggagccaaaaacatcctg 1080
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Db    1154 CAGAACTTGGGCATCAGCCTGGCCAACTTGTTGCTGAGCAAAGGAGCCAAAAACATCCTG 1213

Qy    1081 gatgttgcacggcaattgaacgatgcccattaa 1113
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Db    1214 GATGTTGCACGGCAGCTTAACGATGCCCATTAA 1246
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RESULT   4
HSPBGDR2
LOCUS       HSPBGDR2     1377 bp    mRNA            PRI       06-SEP-1995
DEFINITION  Human mRNA for non-erythropoietic porphobilinogen deaminase
            (hydroxymethylbilane synthase; EC4.3.1.8).
ACCESSION   X04808
VERSION     X04808.1  GI:35308
KEYWORDS    hydroxymethylbilane synthase; porphobilinogen deaminase.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1377)
  AUTHORS   Grandchamp,B., De Verneuil,H., Beaumont,C., Chretien,S., Walter,O.
            and Nordmann,Y.
  TITLE     Tissue-specific expression of porphobilinogen deaminase. Two
            isoenzymes from a single gene
  JOURNAL   Eur. J. Biochem. 162 (1), 105-110 (1987)
  MEDLINE   87133520
COMMENT     Data kindly reviewed (15-SEP-1987) by Grandchamp B.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /cell_type="lymphoblastoid cell"
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                     /note="porphobilinogen deaminase mRNA"
     CDS             28. .1113
                     /note="porphobilinogen deaminase (AA 1-361)"
                     /codon_start=1
                     /protein_id="CAA28499.1"
                     /db_xref="GI:35309"
                     /db_xref="SWISS-PROT:P08397"
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ORIGIN


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  Best Local Similarity   99.5%;  Pred. No. 6.6e-254;
  Matches 1107;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CACACAGCCTACTTTCCAAGCGGAGCCATGTCTGGTAACGGCAATGCGGCTGCAACGGCG 60

Qy      61 gaagaaaacagcccaaagatgagagtgattcgcgtgggtacccgcaagagccagcttgct 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GAAGAAAACAGCCCAAAGATGAGAGTGATTCGCGTGGGTACCCGCAAGAGCCAGCTTGCT 120

Qy     121 cgcatacagacggacagtgtggtggcaacattgaaagcctcgtaccctggcctgcagttt 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CGCATACAGACGGACAGTGTGGTGGCAACATTGAAAGCCTCGTACCCTGGCCTGCAGTTT 180

Qy     181 gaaatcattgctatgtccaccacaggggacaagattcttgatactgcactctctaagatt 240
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Db     181 GAAATCATTGCTATGTCCACCACAGGGGACAAGATTCTTGATACTGCACTCTCTAAGATT 240

Qy     241 ggagagaaaagcctgtttaccaaggagcttgaacatgccctggagaagaatgaagtggac 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GGAGAGAAAAGCCTGTTTACCAAGGAGCTTGAACATGCCCTGGAGAAGAATGAAGTGGAC 300

Qy     301 ctggttgttcactccttgaaggacctgcccactgtgcttcctcctggcttcaccatcgga 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CTGGTTGTTCACTCCTTGAAGGACCTGCCCACTGTGCTTCCTCCTGGCTTCACCATCGGA 360

Qy     361 gccatctgcaagcgggaaaaccctcatgatgctgttgtctttcacccaaaatttgttggg 420
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Db     361 GCCATCTGCAAGCGGGAAAACCCTCATGATGCTGTTGTCTTTCACCCAAAATTTGTTGGG 420

Qy     421 aagaccctagaaaccctgccagagaagagtgtggtgggaaccagctccctgcgaagagca 480
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Qy     481 gcccagctgcagagaaagttcccgcatctggagttcaggagtattcggggaaacctcaac 540
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Qy     541 acccggcttcggaagctggacgagcagcaggagttcagtgccatcatcctggcaacagct 600
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Db     541 ACCCGGCTTCGGAAGCTGGACGAGCAGCAGGAGTTCAGTGCCATCATCCTAGCAACAGCT 600

Qy     601 ggcctgcagcgcatgggctggcacaaccgggttgggcagatcctgcaccctgaggaatgc 660
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Qy     661 atgtatgctgtgggccaggggccttgggcgtggaagtgcgagccaaggaccaggacatc 720
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Qy     721 ttggatctggtgggtgtgctgcacgatcccgagactctgcttcgctgcatcgctgaaagg 780
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Qy     781 gccttcctgaggcacctggaaggaggctgcagtgtgccagtagccgtgcatacagctatg 840
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Db     781 GCCTTCCTGAGGCACCTGGAAGGAGGCTGCAGTGTGCCAGTAGCCGTGCATACAGCTATG 840

Qy     841 aaggatgggcaactgtacctgactggaggagtctggagtctagacggctcagatagcata 900
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Qy     901 caagagaccatgcaggctaccatccatgtccctgcccagcatgaagatggccctgaggat 960
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Qy     961 gacccacagttggtaggcatcactgctcgtaacattccacgagggccccagttggctgcc 1020
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Qy    1021 cagaacttgggcatcagcctggccaacttgttgctgagcaaaggagccaaaaacatcctg 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    1081 gatgttgcacggcaattgaacgatgcccattaa 1113
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Db    1081 GATGTTGCACGGCAGCTTAACGATGCCCATTAA 1113


RESULT   5
HSPBGDR
LOCUS       HSPBGDR      1380 bp    mRNA            PRI       06-SEP-1995
DEFINITION  Human mRNA for porphobilinogen deaminase (PBG-D, EC 4.3.1.8).
ACCESSION   X04217
VERSION     X04217.1  GI:35306
KEYWORDS    deaminase; porphobilinogen deaminase.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1380)
  AUTHORS   Raich,N., Romeo,P.H., Dubart,A., Beaupain,D., Cohen-Solal,M. and
            Goossens,M.
  TITLE     Molecular cloning and complete primary sequence of human
            erythrocyte porphobilinogen deaminase
  JOURNAL   Nucleic Acids Res. 14 (15), 5955-5968 (1986)
  MEDLINE   86312872
COMMENT     Porphobilinogen deaminase is the third enzyme of the heme
            biosynthetic pathway.  Deficiency of this enzyme leads to the
            dominant hereditary disease Acute Intermittent Porphyria (AIP).
FEATURES             Location/Qualifiers
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                     /db_xref="GI:35307"
                     /db_xref="SWISS-PROT:P08397"
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ORIGIN


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Db      63 GGAAGAAAACAGCCCAAAGATGAGAGTGATTCGCGTGGGTACCCGCAAGAGCCAGCTTGC 122
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Qy    120 tcgcatacagacggacagtgtggtggcaacattgaaagcctcgtaccctggcctgcagtt 179
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Qy    180 tgaaatcattgctatgtccaccacaggggacaagattcttgatactgcactctctaagat 239
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Qy    300 cctggttgttcactccttgaaggacctgcccactgtgcttcctcctggcttcaccatcgg 359
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Qy    360 agccatctgcaagcgggaaaaccctcatgatgctgttgtctttcacccaaaatttgttgg 419
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Db    363 AGCCATCTGCAAGCGGGAAAACCCTCATGATGCTGTTGTCTTTCACCCAAAATTTGTTGG 422

Qy    420 gaagaccctagaaaccctgccagagaagagtgtggtgggaaccagctccctgcgaagagc 479
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Db    423 GAAGACCCTAGAAACCCTGCCAGAGAAGAGTGTGGTGGGAACCAGCTCCCTGCGAAGAGC 482

Qy    480 agcccagctgcagagaaagttcccgcatctggagttcaggagtattcggggaaacctcaa 539
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LOCUS       AX020182     1035 bp    DNA             PAT       07-SEP-2000
DEFINITION  Sequence 1 from Patent WO9937325.

ACCESSION   AX020182
VERSION     AX020182.1  GI:10043973
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1035)
  AUTHORS   Fogh,J. and Gellerfors,P.
  TITLE     Method for treating acute intermittent porphyria (aip) and other
            porphyric diseases
  JOURNAL   Patent: WO 9937325-A 1 29-JUL-1999;
            FOGH JENS (DK); HEMEBIOTECH A S (DK); GELLERFORS PAER (SE)
FEATURES             Location/Qualifiers
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  Query Match             93.0%;  Score 1035;  DB 9;  Length 1035;
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RESULT   7
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DEFINITION  Sequence 3 from Patent WO0107065.
ACCESSION   AX079027
VERSION     AX079027.1  GI:13158602
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
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REFERENCE   1  (bases 1 to 1035)
  AUTHORS   Gellerfors,P. and Fogh,J.
  TITLE     Production of rhpbgd and new therapeutic methods for treating
            patients with acute intermittent porphyria (aip) and other
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  JOURNAL   Patent: WO 0107065-A 3 01-FEB-2001;
            Hemebiotech A/S (DK)
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BASE COUNT      250 a    271 c    302 g    212 t
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  Query Match             93.0%;  Score 1035;  DB 10;  Length 1035;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-237;
  Matches 1035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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DEFINITION  Sequence 10 from Patent WO9937325.
ACCESSION   AX020191
VERSION     AX020191.1  GI:10043982
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1260)
  AUTHORS   Fogh,J. and Gellerfors,P.
  TITLE     Method for treating acute intermittent porphyria (aip) and other
            porphyric diseases
  JOURNAL   Patent: WO 9937325-A 10 29-JUL-1999;
            FOGH JENS (DK); HEMEBIOTECH A S (DK); GELLERFORS PAER (SE)
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DEFINITION  Sequence 13 from Patent WO0107065.
ACCESSION   AX079037
VERSION     AX079037.1  GI:13158612
KEYWORDS    .
SOURCE      human.
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REFERENCE   1  (bases 1 to 1260)
  AUTHORS   Gellerfors,P. and Fogh,J.
  TITLE     Production of rhpbgd and new therapeutic methods for treating
            patients with acute intermittent porphyria (aip) and other
            porphyric diseases
  JOURNAL   Patent: WO 0107065-A 13 01-FEB-2001;
            Hemebiotech A/S (DK)
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ORIGIN

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Qy     499 ttcccgcatctggagttcaggagtattcggggaaacctcaacacccggcttcggaagctg 558
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Qy    679 ggggccttgggcgtggaagtgcgagccaaggaccaggacatcttggatctggtgggtgtg 738
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Db    731 GGGGCCTTGGGCGTGGAAGTGCGAGCCAAGGACCAGGACATCTTGGATCTGGTGGGTGTG 790

Qy    739 ctgcacgatcccgagactctgcttcgctgcatcgctgaaagggccttcctgaggcacctg 798
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Qy    799 gaaggaggctgcagtgtgccagtagccgtgcatacagctatgaaggatgggcaactgtac 858
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RESULT 10
AX020190/c
LOCUS       AX020190     3988 bp    DNA             PAT       07-SEP-2000
DEFINITION  Sequence 9 from Patent WO9937325.
ACCESSION   AX020190
VERSION     AX020190.1  GI:10043981
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3988)
  AUTHORS   Fogh,J. and Gellerfors,P.
  TITLE     Method for treating acute intermittent porphyria (aip) and other
            porphyric diseases
  JOURNAL   Patent: WO 9937325-A 9 29-JUL-1999;
            FOGH JENS (DK); HEMEBIOTECH A S (DK); GELLERFORS PAER (SE)
FEATURES             Location/Qualifiers
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BASE COUNT      918 a   1056 c   1000 g   1014 t
ORIGIN


  Query Match             93.0%;  Score 1035;  DB 9;  Length 3988;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-237;
  Matches 1035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     79 atgagagtgattcgcgtgggtacccgcaagagccagcttgctcgcatacagacggacagt 138
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Qy    799 gaaggaggctgcagtgtgccagtagccgtgcatacagctatgaaggatgggcaactgtac 858
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Qy   1099 aacgatgcccattaa 1113
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RESULT 11
AX079036/c
LOCUS       AX079036     3988 bp    DNA             PAT       22-FEB-2001
DEFINITION  Sequence 12 from Patent WO0107065.
ACCESSION   AX079036
VERSION     AX079036.1  GI:13158611
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KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3988)
  AUTHORS   Gellerfors,P. and Fogh,J.
  TITLE     Production of rhpbgd and new therapeutic methods for treating
            patients with acute intermittent porphyria (aip) and other
            porphyric diseases
  JOURNAL   Patent: WO 0107065-A 12 01-FEB-2001;
            Hemebiotech A/S (DK)
FEATURES             Location/Qualifiers
     source          1. .3988
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BASE COUNT      918 a   1056 c   1000 g   1014 t
ORIGIN


  Query Match           93.0%;  Score 1035;  DB 10;  Length 3988;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-237;
  Matches 1035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT  12
AX020183
LOCUS       AX020183     1035 bp    DNA             PAT       07-SEP-2000
DEFINITION  Sequence 2 from Patent WO9937325.
ACCESSION   AX020183
VERSION     AX020183.1  GI:10043974
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1035)
  AUTHORS   Fogh,J. and Gellerfors,P.
  TITLE     Method for treating acute intermittent porphyria (aip) and other
            porphyric diseases
  JOURNAL   Patent: WO 9937325-A 2 29-JUL-1999;
            FOGH JENS (DK); HEMEBIOTECH A S (DK); GELLERFORS PAER (SE)
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ORIGIN


  Query Match           92.8%;  Score 1033.4;  DB 9;  Length 1035;
  Best Local Similarity  99.9%;  Pred. No. 4e-237;
  Matches 1034;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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RESULT  13
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LOCUS       AX020184     1035 bp    DNA             PAT       07-SEP-2000
DEFINITION  Sequence 3 from Patent WO9937325.
ACCESSION   AX020184
VERSION     AX020184.1  GI:10043975
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1035)
  AUTHORS   Fogh,J. and Gellerfors,P.
  TITLE     Method for treating acute intermittent porphyria (aip) and other
            porphyric diseases
  JOURNAL   Patent: WO 9937325-A 3 29-JUL-1999;
            FOGH JENS (DK); HEMEBIOTECH A S (DK); GELLERFORS PAER (SE)
FEATURES             Location/Qualifiers
     source          1. .1035
                     /organism="unidentified"
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BASE COUNT      250 a    271 c    303 g    211 t

ORIGIN


  Query Match           92.8%;  Score 1033.4;  DB 9;  Length 1035;
  Best Local Similarity  99.9%;  Pred. No. 4e-237;
  Matches 1034;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy    139 gtggtggcaacattgaaagcctcgtaccctggcctgcagtttgaaatcattgctatgtcc 198
Db     61 GTGGTGGCAACATTGAAAGCCTCGTACCCTGGCCTGCAGTTTGAAATCATTGCTATGTCC 120

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REFERENCE   1  (bases 1 to 1035)
  AUTHORS   Gellerfors,P. and Fogh,J.
  TITLE     Production of rhpbgd and new therapeutic methods for treating
            patients with acute intermittent porphyria (aip) and other
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  JOURNAL   Patent: WO 0107065-A 5 01-FEB-2001;
            Hemebiotech A/S (DK)
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ORIGIN


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DEFINITION  Sequence 6 from Patent WO0107065.
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VERSION     AX079030.1  GI:13158605
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REFERENCE   1  (bases 1 to 1035)
  AUTHORS   Gellerfors,P. and Fogh,J.
  TITLE     Production of rhpbgd and new therapeutic methods for treating
            patients with acute intermittent porphyria (aip) and other
            porphyric diseases
  JOURNAL   Patent: WO 0107065-A 6 01-FEB-2001;
            Hemebiotech A/S (DK)
FEATURES             Location/Qualifiers
     source          1. .1035
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BASE COUNT      250 a    271 c    303 g    211 t
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